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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:43:38 ; Search time 43 Seconds

(without alignments)

387.134 Million cell updates/sec

Title: US-10-723-123-3

Perfect score: 1194

Sequence: 1 MPLNLGDSFPDFOAALGAE.....EALQLPSGKPYRLTTPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	223	3	US-09-411-578-3
2	1194	100.0	223	4	US-09-749-233-3
3	640.5	53.6	235	3	US-08-862-540-9
4	640.5	53.6	235	3	US-09-633-043-9
5	637.5	53.4	223	4	US-09-538-092-1038
6	618.5	51.8	235	3	US-08-862-540-2
7	618.5	51.8	235	3	US-09-633-043-2
8	498.5	41.8	224	4	US-09-270-767-43949
9	497.5	41.7	222	4	US-09-252-991A-16816
10	494.5	41.4	216	4	US-09-328-352-5328
11	453	37.9	257	4	US-09-248-796A-20366
12	413.5	34.6	161	4	US-09-202-329-15
13	256.5	21.5	116	4	US-09-270-767-43977
14	222	18.6	184	4	US-09-902-540-10665
15	205	17.2	194	4	US-09-202-329-10
16	199	16.7	982	4	US-09-551-974A-95
17	199	16.7	982	4	US-09-565-501A-95
18	199	16.7	982	4	US-09-639-206A-95
19	199	16.7	982	4	US-09-874-923-95
20	199	16.7	1427	4	US-09-551-974A-97
21	199	16.7	1427	4	US-09-565-501A-97
22	199	16.7	1427	4	US-09-639-206A-97
23	199	16.7	1427	4	US-09-874-923-97
24	199	16.7	1641	4	US-09-551-974A-96
25	199	16.7	1641	4	US-09-565-501A-96
26	199	16.7	1641	4	US-09-639-206A-96
27	199	16.7	1641	4	US-09-874-923-96

28	196.5	16.5	195	4	US-09-556-877-65	Sequence 65, Appl
29	196.5	16.5	195	4	US-09-620-412C-65	Sequence 65, Appl
30	196.5	16.5	195	4	US-09-410-568-65	Sequence 65, Appl
31	196.5	16.5	195	4	US-09-598-419-65	Sequence 65, Appl
32	196.5	16.5	196	4	US-09-556-877-294	Sequence 294, App
33	196.5	16.5	196	4	US-09-620-412C-294	Sequence 294, App
34	196.5	16.5	196	4	US-09-598-419-294	Sequence 294, App
35	196.5	16.5	202	4	US-09-556-877-92	Sequence 92, Appl
36	196.5	16.5	202	4	US-09-620-412C-92	Sequence 92, Appl
37	196.5	16.5	202	4	US-09-410-568-92	Sequence 92, Appl
38	196.5	16.5	202	4	US-09-598-419-92	Sequence 92, Appl
39	193.5	16.2	195	4	US-08-311-731A-84	Sequence 84, Appl
40	193	16.2	231	4	US-09-438-185A-780	Sequence 780, App
41	192.5	16.1	198	4	US-09-202-329-13	Sequence 13, Appl
42	191	16.0	199	2	US-08-467-265-17	Sequence 17, Appl
43	191	16.0	199	3	US-08-467-265-17	Sequence 17, Appl
44	191	16.0	199	3	US-09-407-891-17	Sequence 17, Appl
45	189	15.8	204	4	US-09-252-991A-17611	Sequence 17611, A

ALIGNMENTS

RESULT 1

US-09-411-578-3
; Sequence 3, Application US/09411578
; Patent No. 6203801
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaa
; CURRENT APPLICATION NUMBER: US/09/411,578
; CURRENT FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 98203384.7
; EARLIER FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: 98203457.1
; EARLIER FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Elmeria tenella
US-09-411-578-3

Query Match	100.0%;	Score 1194;	DB 3;	Length 223;
Best Local Similarity	100.0%;	Pred. No. 6.2e-133;		
Matches 223;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	MPLNLGDSFPDFOAALGAEHRLHLYLGD	SWGWMF	SHPNDFTPVCTT
Db	1	MPLNLGDSFPDFOAALGAEHRLHLYLGD	SWGWMF	SHPNDFTPVCTT
Qy	61	TKNKCKLVGFCNDLQSHREWAKDINAYAG	RGNLFPPLVCDN	RELAASLGIMDPAEKD
Db	61	TKNKCKLVGFCNDLQSHREWAKDINAYAG	RGNLFPPLVCDN	RELAASLGIMDPAEKD
Qy	121	KKGLPLTCRCVFFISPEKKLAASILYPAT	TGGRNFABILRV	LDLSQLTAKFPVATPDWTA
Db	121	KKGLPLTCRCVFFISPEKKLAASILYPAT	TGGRNFABILRV	LDLSQLTAKFPVATPDWTA
Qy	181	GAKCCVVPNLAAEEAQRLLPKGHEALQL	PSGKPYRLTTP	DPGRG 223
Db	181	GAKCCVVPNLAAEEAQRLLPKGHEALQL	PSGKPYRLTTP	DPGRG 223

RESULT 2

US-09-749-233-3
; Sequence 3, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:

```
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/411,578
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Eimeria tenella
US-09-749-233-3

Query Match      100.0%; Score 1194; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.2e-133;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M P L N L G D S P D F Q A E A L G A E H F R L H E Y L G D S W G V M F S H P N D F T P V C T T T E L A E A V K L Q D S F 60
D b 1 M P L N L G D S P D F Q A E A L G A E H F R L H E Y L G D S W G V M F S H P N D F T P V C T T T E L A E A V K L Q D S F 60

QY 61 T K N C K L V G F S C N D L Q S H R E W A K D I M A Y A G R S G N L P P L V C D P N R E L A A S L G I M D P A E K D 120
D b 61 T K N C K L V G F S C N D L Q S H R E W A K D I M A Y A G R S G N L P P L V C D P N R E L A A S L G I M D P A E K D 120

QY 121 K G L P L T C R C V F F I S P E K K L A A S I L Y P A T T G R N F A S I L R V L D S L Q L T A K F P V A T P V D W T A 180
D b 121 K G L P L T C R C V F F I S P E K K L A A S I L Y P A T T G R N F A S I L R V L D S L Q L T A K F P V A T P V D W T A 180

QY 181 G A K C C V V P N L A E A Q R L L P K G H E A L Q L P S G K P Y L R L T P D P R G 223
D b 181 G A K C C V V P N L A E A Q R L L P K G H E A L Q L P S G K P Y L R L T P D P R G 223

RESULT 3
US-08-862-540-9
; Sequence 9, Application US/08862540
; Patent No. 6150135
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Tsuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,540
; FILING DATE: MAY 23, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-540-9

Query Match      53.6%; Score 640.5; DB 3; Length 235;
Best Local Similarity 55.5%; Pred. No. 2.5e-67;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY 5 L G D S P D F Q A E A L G A E H F R L H E Y L G - D S M G V M F S H P N D F T P V C T T E L A E A V K L Q D S F T K K 63
D b 7 L G D K F P D Q A E T S E S F I S S F H D W I G K S W A I L F S H P R D F T P V C T T E L A R I V L Q E P E F K K R 66

QY 64 N C K L V G F S C N D L Q S H R E W A K D I M A Y A G R ----- S G N - L P F P L V C D P N R E L A A S L G I 113
D b 67 N V K L I G L S C D S V Q S H R K W A D D I I E L C R M K S G D S N T C C S G N K L P F P I A D D N R S L A S K L G M 126

QY 114 M P A E K D K G L P L T C R C V F F I S P E K K L A A S I L Y P A T T G R N F A E I L R V L D S L Q L T A K F P V A 173
D b 127 M P D E C D E G A A L T A R C L F I I G P E K L K L S I L Y P A T T G R N F D E I L R V D S L Q L T A T K L V A 186

QY 174 T P V D W T A G A C C V V P N L A E A Q R L L P K G H E A L Q L P S G K P Y L R L T P D P R 222
D b 187 T P V D M Q N G D C V V P T I N D N E A K L F G E K I N T V E L P S G K R Y L R M V A H P K 235

RESULT 4
US-09-633-043-9
; Sequence 9, Application US/09633043
; Patent No. 6352836
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Tsuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/633,043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/862,540
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-633-043-9

Query Match      53.6%; Score 640.5; DB 3; Length 235;
Best Local Similarity 55.5%; Pred. No. 2.5e-67;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY 5 LGDSFPDFOAEALGAEHFRLHEYLGD-SWGVMFSDHNDFTPVCTTELAEAVKLQDSFTKK 63
Db 7 LGDFPDPQATSSFSFSSFDWIGKDSWAILFSDHNDFTPVCTTELAARLVQLAPEPKR 66

QY 64 NCKLVGFCNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASIGI 113
Db 67 NVKLIGLSCDSVQSHRWADDIIELCRMKSGDSNTCCSGNKLFPPIADNRSLSKLG 126

QY 114 MDPAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
Db 127 MDPDECDEKGAALTARCLFIIGPEKTLKLSILYPATTGRNFDILRVVDSIQLTAVKLA 186

QY 174 TPVDWTAGKCCVVPNLAAEAQRLLPKGHEALQPSGKPYRLTPDPR 222
Db 187 TPVDWQNGDDCVVVPNTINDNEAKKLFGEKINTIPELPSGKPYRLMVAHPK 235

RESULT 5
US-09-538-092-1038
; Sequence 1038, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformatter Version 0.9
; SEQ ID NO 1038
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P30041
US-09-538-092-1038

Query Match      53.4%; Score 637.5; DB 4; Length 223;
Best Local Similarity 56.6%; Pred. No. 5.3e-67;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;

QY 3 LNLGDSFPDFOAEALGAEHFRLHEYLGD-SWGVMFSDHNDFTPVCTTELAEAVKLQDSFTK 62
Db 4 LLLGDVAPNFEANTT-VGRIRFHDGLDGSWILFSDHNDFTPVCTTELAGRAAKLAPEFAK 62

QY 63 KCKLVGFCNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASIGIMDPAEKD 120
Db 63 RNVKLIASLSDSVEDHLAWSKDINAYNCEPTEKLPPIIDDRNRELAAILLGMIDPAEKD 122

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPPVDWTA 180
Db 123 EKGMPVTVAVVFGPDKCLKLSILYPATTGRNFDILRVVISIQLTAEKRVATPVDWMD 182

QY 181 GAKCCVVPNLAAEAQRLLPKGHEALQPSGKPYRLTPDPR 221
Db 183 GDSVMVLPITPEEAKKLFPGVFTKELPSGKPYRLTPQP 223
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RESULT 6
US-08-862-540-2
; Sequence 2, Application US/08862540
; Patent No. 6150135
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
; APPLICANT: Naotoshi Teuji
; TITLE OF INVENTION: DIROFILARIA AND BRUGIA THIOREDOXIN
; TITLE OF INVENTION: PEROXIDASE TYPE-2 (TPX-2) PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, AND USES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Hesk Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA: US/08/862,540
; APPLICATION NUMBER: US/08/862,540
; FILING DATE: MAY 23, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-540-2

Query Match      51.8%; Score 618.5; DB 3; Length 235;
Best Local Similarity 54.1%; Pred. No. 1e-64;
Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;

QY 5 LGDSFPDFOAEALGAEHFRLHEYLGD-SWGVMFSDHNDFTPVCTTELAEAVKLQDSFTKK 63
Db 7 LGDFPDPQATSSFSFSSFDWIGKDSWAILFSDHNDFTPVCTTELAARLVQLAPEPKR 66

QY 64 NCKLVGFCNDLQSHREWAKDIMAYAGR-----SGN-LPPPLVCDPNRELAASIGI 113
Db 67 NVKLIGLSCDSVQSHRWADDIINAVCKMKCNDGDTCCSGNKLFPPIADNRSFLATELGM 126

QY 114 MDPAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
Db 127 MDPDERDENGALTARCVFIIGPEKTLKLSILYPATTGRNFDILRVVDSIQLTAVKLA 186

QY 174 TPVDWTAGKCCVVPNLAAEAQRLLPKGHEALQPSGKPYRLTPDPR 222
Db 187 TPVDWQNGDDCVVVPNTINDTEAKKLFGEKINTIPELPSGKPYRLMVAHPK 235

RESULT 7
US-09-633-043-2
; Sequence 2, Application US/09633043
; Patent No. 6352836
; GENERAL INFORMATION:
; APPLICANT: Ramaswamy Chandrashekar
```



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; Sequence 5328, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5328
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5328

Query Match      41.4%; Score 494.5; DB 4; Length 216;
Best Local Similarity 45.7%; Pred. No. 4.4e-50;
Matches 102; Conservative 37; Mismatches 69; Indels 15; Gaps 6;

Qy 1 MPLNLGDSFPDFOAEAL-GAEHFRHLHYLGDSWGMFSPHNDFTPVCTTELAEAVKLQDS 59
Db 4 MTLRLGDTAPDFQESSEGTINF--YDFLGDSWGLFSHPADYTPVCTTELGYTAKLKDE 61

Qy 60 FTKGNCKLVGSCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEK 119
Db 62 FEKRNKAIASLVDDVESHKGWINDINETQNTTVN--FPITADKDRKVSLEYGFHPNAS 119

Qy 120 DKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAETLRVLSLQLTAKFPVATPDWT 179
Db 120 E-----TLTVRLVLDIPNKKVRLIITYPASTGRNFNEVLRVDSLQTDKHKVATPANWQ 175

Qy 180 AGAKCCVVPNLIA-AEEAQRLLPKGHEALQLPSPKPYRLRLTPDP 221
Db 176 QGEDVWLVPSLKDEEIKQRPFGYTVV-----KPYRLRLTPQ 213

RESULT 11
US-09-248-796A-20366
; Sequence 20366, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20366
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20366

Query Match      37.9%; Score 453; DB 4; Length 257;
Best Local Similarity 41.8%; Pred. No. 4.7e-45;
Matches 92; Conservative 42; Mismatches 74; Indels 12; Gaps 5;

Qy 3 LNLGDSFPDFOAEALGAEHFRHLHYLGDSWGMFSPHNDFTPVCTTELAEAVKLQDSFTK 62
Db 41 LRVGSTAPDFKADTTNG-HILFHEYIGDRWGLFSHPAANTSVCSLSAFARLEPEFTK 99

Qy 63 KNCKLVGSCNDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEK-- 119
Db 100 RGVKLLAISADPVEANSWDIDMEDFSG--SRVKFPPIIADPERKVATLYDMIDHQDATNL 157

Qy 120 DKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAETLRVLSLQLTAKFPVATPDWT 179
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Db 158 DDKGLQLTIRAVFIIDPSKIRLIMTYPASTGRNTAEVLRVLSLQLVDRKQKVITPINWV 217
Qy 180 AGAKCCVVPNLIAAEEAQRLLPKGHEALQLPSPKPYRLRLTP 219
Db 218 PGDDVLVHMGVDPDEARVLPFK-YRAI-----KPYIRLTP 251

RESULT 12
US-09-202-329-15
; Sequence 15, Application US/09202329A
; Patent No. 6676944
; GENERAL INFORMATION:
; APPLICANT: Dalton, John P
; APPLICANT: Andrews, Stuart J
; TITLE OF INVENTION: Vaccine containing a piroxiredoxin and/or a B-tubulin
; FILE REFERENCE: 1181-243
; CURRENT APPLICATION NUMBER: US/09/202,329A
; CURRENT FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: GB 9612214.8
; EARLIER FILING DATE: 1996-06-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01573
; EARLIER FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 15
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Onchocerca volvulus
; PUBLICATION INFORMATION:
; TITLE: GenBank accession no. U09385
US-09-202-329-15

Query Match      34.6%; Score 413.5; DB 4; Length 161;
Best Local Similarity 51.9%; Pred. No. 1.1e-40;
Matches 83; Conservative 20; Mismatches 50; Indels 7; Gaps 1;

Qy 60 FTKGNCKLVGSCNDLQSHREWAKDIMAY-----AGRSNGLPPLVCDPNRELAASLG 112
Db 2 FKRNKVLIGLSCDSADSHSKWADDILALYKMKVCGCDSEKCLPYPIADEDRSLATELG 61

Qy 113 IMDPAEKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAETLRVLSLQLTAKFPV 172
Db 62 MMDPDERDEKGNLTARCVFIIGSDKTLKLSILYPATTGRNFDSEILRVDSLQLTAVKLV 121

Qy 173 ATPVDVDTAGAKCCVVPNLAAEEAQRLLPKGHEALQLPSPGK 212
Db 122 ATPVDWKGDDCVVLPTDIDNEAKKLFGEKIHIDLPSPGK 161

RESULT 13
US-09-270-767-43977
; Sequence 43977, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43977
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43977

Query Match      21.5%; Score 256.5; DB 4; Length 116;
Best Local Similarity 46.4%; Pred. No. 2.6e-22;
Matches 51; Conservative 20; Mismatches 38; Indels 1; Gaps 1;

Qy 110 SLGIMDPAEKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAETLRVDSLQLTAK 169
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Db 4 SLGMLDEEQKQPEVGVKTIKIRALFIISPDHKVRLSMFPMSTGRVNDVDEILRTIDSLQITDR 63
Qy 170 FP-VATPDVWTAGACCCVNVNLAEEAQRLLPKGHEALQLPSGKPYRLT 218
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 LKVATPANWTGTVKVMILPTVTDEEAHKLFPKGFVKVSMPSGVNVYVRT 113

RESULT 14
US-09-902-540-10665
; Sequence 10665, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10665
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10665

Query Match 18.6%; Score 222; DB 4; Length 184;
Best Local Similarity 31.9%; Pred. No. 6.5e-18;
Matches 60; Conservative 29; Mismatches 73; Indels 26; Gaps 7;

Qy 3 LNLGDSPPDQAEAL-----GAHFRL-HEYLGDGSGVMFSPNDFTPVCTTTELAEAVKL 56
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 LTVGDKIPNFKVATVSLKSGKGFQDITNETFKGKMLVLPFWPKDFTFICTEIAEFGKK 61

Qy 57 QDSFTKKNKLVGSCNDLQSHREWA---KDIWAYAGRSNLPFPPLVCDPNRELAASLGI 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 NKDFTDRDAQVLGLSTDSEFVHAWRTHPPDLK-----NLPPFPLADIKHELNALGI 114

Qy 114 MDPAEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVA 173
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 LHKEE-----GVAL--RATFIADPEGIIRHVTVNDLSVGRNVSETIRLDALQDTE---L 164

Qy 174 TPVDWTAG 181
    |||||
Db 165 CPCNWTGK 172

RESULT 15
US-09-202-329-10
; Sequence 10, Application US/09202329A
; Patent No. 6676944
; GENERAL INFORMATION:
; APPLICANT: Dalton, John P
; APPLICANT: Andrews, Stuart J
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin
; FILE REFERENCE: 1181-243
; CURRENT APPLICATION NUMBER: US/09/202,329A
; CURRENT FILING DATE: 1999-02-19
; EARLIER APPLICATION NUMBER: GB 9612214.8
; EARLIER FILING DATE: 1996-06-11
; EARLIER APPLICATION NUMBER: PCT/GB97/01573
; EARLIER FILING DATE: 1997-06-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Fasciola hepatica
US-09-202-329-10
```

```
Query Match 17.2%; Score 205; DB 4; Length 194;
Best Local Similarity 27.6%; Pred. No. 7.3e-16;
Matches 55; Conservative 36; Mismatches 86; Indels 22; Gaps 6;

Qy 10 PDFQAEALGAHFRL-----LHEYLGDGSGVMFSPNDFTPVCTTTELAEAVKLQDSFTKKNCK 66
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 PNFSGQAVVGKFEFETISLSDYKG-KWVILAFYPLDFTFVCTTEIIAISIQMEQFAQRNCA 67

Qy 67 LVGFCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKDKGLPL 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 VIFCSTDSVYSHLQWTK-MDRKVGIGQLNFPPLADKNMVSRAFGVLDEEQGN----- 120

Qy 127 TCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDWTAGAKCCV 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 TYRGNFLIDPKGVLQITVNDPVGSRVBEALRLDLDAFIHBEHGEVCPANWPKSK-TI 179

Qy 187 VPNLAEEAQRLLPKGHEA 205
    |||||
Db 180 VPT-----PDGSKA 188

RESULT 16
US-09-551-974A-95
; Sequence 95, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 982
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-95

Query Match 16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

Qy 10 PDFQAEAL-----GAHFRLHEYLGDGSGVMFSPNDFTPVCTTTELAEAVKLQDS---FTK 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 PSFEEVALMPNGSFKKISLSSYKG-KWVVLFFYPPLDFTFVCPTEV---IAPSDSVSRFNE 75

Qy 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKDKK 122
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 LNCEVLACSIDSSEYAHQLQWTLQDRKKGK-LGTWAIPLADTKTSIARSYGVLEESQ---- 130

Qy 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSQLTAKFPVATPDVDTAGA 182
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 131 --GVAYRGLFIDPHGNLRQITVNDMPVGRSVEEVRLLEAFQFVEKHGEVCPANWKKGA 188

Qy 183 KCC-VVPNLAEE-----EAQRLLPKGHE 204
    |||||
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 17
US-09-565-501A-95
; Sequence 95, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
```

APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Peter Probst
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
FILE REFERENCE: 210121.42067
CURRENT APPLICATION NUMBER: US/09/565.501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 982
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
Leishmania antigens
US-09-565-501A-95

Query Match 16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;
QY 10 PDFQAEAL-----GAEHFRLHLYLGDGSGVGFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
Db 20 PSFEVALMPNGSPFKISLSYKG-KWVLFYFPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEVLRLLEAFQVKEHGEVCPANWKGA 188
QY 183 KCC-VVNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 18
US-09-639-206A-95
Sequence 95, Application US/09639206A
Patent No. 6613337
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
FILE REFERENCE: 210121.42067
CURRENT APPLICATION NUMBER: US/09/639.206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 982
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
Leishmania antigens
US-09-639-206A-95

Query Match 16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;
QY 10 PDFQAEAL-----GAEHFRLHLYLGDGSGVGFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
Db 20 PSFEVALMPNGSPFKISLSYKG-KWVLFYFPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEVLRLLEAFQVKEHGEVCPANWKGA 188
QY 183 KCC-VVNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

RESULT 19
US-09-874-923-95
Sequence 95, Application US/09874923
Patent No. 6638517
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
FILE REFERENCE: 210121.42068
CURRENT APPLICATION NUMBER: US/09/874.923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 982
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
Leishmania antigens
US-09-874-923-95

Query Match 16.7%; Score 199; DB 4; Length 982;
Best Local Similarity 27.4%; Pred. No. 4.7e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;
QY 10 PDFQAEAL-----GAEHFRLHLYLGDGSGVGFSPHNDFTPVCTTTELAAVAKLQDS---FTK 62
Db 20 PSFEVALMPNGSPFKISLSYKG-KWVLFYFPLDFTVCPTTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCEVLACSIDSEYAHLOWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDMWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEVLRLLEAFQVKEHGEVCPANWKGA 188
QY 183 KCC-VVNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKGNE 220

```
RESULT 20
US-09-551-974A-97
; Sequence 97, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551,974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEA VKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPFLDFTVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASPKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLDQRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDWDTA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCPCANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATELKNKGNE 220

; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-97

RESULT 21
US-09-565-501A-97
; Sequence 97, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEA VKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPFLDFTVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASPKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLDQRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDWDTA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCPCANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATELKNKGNE 220

; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEA VKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPFLDFTVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASPKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLDQRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDWDTA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCPCANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATELKNKGNE 220

; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97
```

```
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEA VKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPFLDFTVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASPKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLDQRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDWDTA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCPCANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATELKNKGNE 220

; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL-----GAHFRLHEYLGDGSGWMFSPNDFTPVCTTELAEA VKLQDS---FTK 62
DB 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFYPFLDFTVCPTFV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPASPKDKK 122
DB 76 LNCEVLACSIDSEYAHLOWTLDQRKKG-LGTWAIPLADTKTSIARSYGVLEESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDWDTA 182
DB 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVVEVLRLLEAFQFVEKHGVCPCANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
DB 189 PTMKPEPNASVEGYFSKQSGMDATELKNKGNE 220

; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-97
```



```

RESULT 23
US-09-874-923-97
; Sequence 97, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874, 923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-874-923-97

Query Match      16.7%; Score 199; DB 4; Length 1427;
Best Local Similarity 27.4%; Pred. No. 8.4e-14;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDGSGVMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFPLDFTVCPTFTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVLAACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKNGE 220

RESULT 24
US-09-551-974A-96
; Sequence 96, Application US/09551974A
; Patent No. 6500437
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C5
; CURRENT APPLICATION NUMBER: US/09/551, 974A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-551-974A-96

Query Match      16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDGSGVMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFPLDFTVCPTFTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVLAACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKNGE 220

RESULT 25
US-09-565-501A-96
; Sequence 96, Application US/09565501A
; Patent No. 6607731
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Peter Probst
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C6
; CURRENT APPLICATION NUMBER: US/09/565, 501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-565-501A-96

Query Match      16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDGSGVMFSPNDFTPVCTTTELAEAVKLQDS----FTK 62
Db 20 PSFEEVALMPNGSFKKISLSYKG-KWVVLFFPLDFTVCPTFTEV---IAFSDSVSRFNE 75
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVLAACSIDSEYAHQWTLQDRKKG-LGTWAIPLADTKTSIARSYGVLESQ---- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATGRNFAEILRVLDLSLQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGEVCPANWKKA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMDATLKNKNGE 220

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Db 189 PTMKPEPNASVEGYFSKQSGMSDTELKKNKGNE 220

RESULT 26
US-09-639-206A-96
; Sequence 96, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
; OTHER INFORMATION: Leishmania antigens
US-09-639-206A-96

Query Match 16.7%; Score 199; DB 4; Length 1641;
Best Local Similarity 27.4%; Pred. No. 1e-13;
Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDWSGMFMSHPNDFTPVCTTELAEAVKLQDS---FTK 62
Db 20 PSFEVALMPNGSFKKISLSSYKG-KWVVLFFYPDLDFVCPTFV---IAFSDSVSRFNE 75
QY 63 KCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVLACSIDSEYAHLOWTLQDRKKG-LGTMAIPMLADTKTSIARSYGVLEESQ--- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLDLSQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGVCPCPNWKKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMSDTELKKNKGNE 220

RESULT 27
US-09-874-923-96
; Sequence 96, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; FILE REFERENCE: 210121.420C8
; CURRENT APPLICATION NUMBER: US/09/874,923
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 122

US-09-639-206A-96
; Query Match 16.7%; Score 199; DB 4; Length 1641;
; Best Local Similarity 27.4%; Pred. No. 1e-13;
; Matches 58; Conservative 35; Mismatches 91; Indels 28; Gaps 8;

QY 10 PDFQAEAL----GAEHFRLHEYLGDWSGMFMSHPNDFTPVCTTELAEAVKLQDS---FTK 62
Db 20 PSFEVALMPNGSFKKISLSSYKG-KWVVLFFYPDLDFVCPTFV---IAFSDSVSRFNE 75
QY 63 KCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKDKK 122
Db 76 LNCVLACSIDSEYAHLOWTLQDRKKG-LGTMAIPMLADTKTSIARSYGVLEESQ--- 130
QY 123 GLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLDLSQLTAKFPVATPVDWTAGA 182
Db 131 --GVAYRGLFIIDPHGMLRQITVNDMPVGRSVEEVLRLLEAFQFVEKHGVCPCPNWKKGA 188
QY 183 KCC-VVPNLAAE-----EAQRLLPKGHE 204
Db 189 PTMKPEPNASVEGYFSKQSGMSDTELKKNKGNE 220

US-09-556-877-65
; Query Match 16.5%; Score 196.5; DB 4; Length 195;
; Best Local Similarity 29.6%; Pred. No. 7.5e-15;
; Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

QY 5 LGDSFPDFQAEAL--GAE-HFRLHEYLGDWSGMFMSHPNDFTPVCTTEL-AEAVKLQDSF 60
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLPFPYKDFTVVCTTELHAFQDLVD-F 62
QY 61 TKNCKLVGFCNDLQSHREW---AKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPA 117
Db 63 EEHGAUVLGCSVDIETHSRWLTVD---AGGIEGTETPLADSPKISEAFGLNPE 118
QY 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLDLSQLTAKFPVATPVD 177
Db 119 GS-----LALRATPLIDKHGVRHVRVINDPLGRISIDBELRLDLSLIFFNHGMVCPAN 172
QY 178 WTAGAK 183
Db 173 WRSGER 178

US-09-556-877-65
; Query Match 16.5%; Score 196.5; DB 4; Length 195;
; Best Local Similarity 29.6%; Pred. No. 7.5e-15;
; Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

QY 5 LGDSFPDFQAEAL--GAE-HFRLHEYLGDWSGMFMSHPNDFTPVCTTEL-AEAVKLQDSF 60
Db 5 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLPFPYKDFTVVCTTELHAFQDLVD-F 62
QY 61 TKNCKLVGFCNDLQSHREW---AKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPA 117
Db 63 EEHGAUVLGCSVDIETHSRWLTVD---AGGIEGTETPLADSPKISEAFGLNPE 118
QY 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLDLSQLTAKFPVATPVD 177
Db 119 GS-----LALRATPLIDKHGVRHVRVINDPLGRISIDBELRLDLSLIFFNHGMVCPAN 172
QY 178 WTAGAK 183
Db 173 WRSGER 178
```



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Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 36
US-09-620-412C-92
; Sequence 92, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHLYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPA 117
Db 70 EEHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLDADPSFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNPAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLIDSLIFFENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 37
US-09-410-568-92
; Sequence 92, Application US/09410568
; Patent No. 6555115
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fang, Hang
; APPLICANT: Jen, Shyian
; APPLICANT: Stromberg, Erica Jean
; APPLICANT: Enghart, Susan E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C2
; CURRENT APPLICATION NUMBER: US/09/410,568
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-410-568-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHLYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPA 117
Db 70 EEHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLDADPSFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNPAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLIDSLIFFENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 38
US-09-598-419-92
; Sequence 92, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 92
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Chlamydia
US-09-598-419-92

Query Match 16.5%; Score 196.5; DB 4; Length 202;
Best Local Similarity 29.6%; Pred. No. 7.9e-15;
Matches 55; Conservative 37; Mismatches 75; Indels 19; Gaps 8;

Qy 5 LGDSFPDFOAEAL--GAE-HFRLHLYLGDWGMFHPNDFTPVCTTEL-AEAVKLODSF 60
Db 12 VGRQAPDFSGKAVVCGEKEISLADFRG-KYVVLFFYPKDFTYVCPTELHAFQDRLVD-F 69

Qy 61 TTKNCKLVGFSNCDLQSHREW---AKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPA 117
Db 70 EEHGAVVLGCVDDIETHSRWLTWARD---AGGIEGTEYPLLDADPSFKISEAFGLNPE 125

Qy 118 EKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNPAEILRVLDLSQLTAKFPVATPVD 177
Db 126 GS-----LALRATFLIDKHGVRHAVINDPLGRSIDELRLIDSLIFFENHGMVCPAN 179

Qy 178 WTAGAK 183
Db 180 WRSGER 185

RESULT 39
US-08-311-731A-84
; Sequence 84, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
```


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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:31:58 ; Search time 174 Seconds
(without alignments)
656.285 Million cell updates/sec

Title: US-10-723-123-3
Perfect score: 1194
Sequence: 1 MPLNLGDSFPDFOAEALGAE.....EALQLPSGKPYLRLTPDP 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707	59.2	224	2	Q962X0 toxoplasma
2	668.5	56.0	223	1	PDX6 RAT
3	652.5	54.6	223	1	PDX6 BOVIN
4	645.5	54.1	224	2	Q9TSX9
5	644	53.9	220	2	Q7RGR1
6	644	53.9	220	2	Q86SB3
7	640.5	53.6	227	2	Q6AOD0
8	640.5	53.6	235	2	Q9USA0
9	639.5	53.6	223	1	PDX6 MOUSE
10	637.5	53.4	223	1	PDX6 HUMAN
11	636	53.3	220	2	Q8IAM2
12	636	53.3	220	2	Q9XXW9
13	634	53.1	222	2	Q6PRK9
14	628	52.6	224	2	Q7SYT1
15	625.5	52.4	217	2	Q966Y9
16	621	52.0	224	2	Q6P624
17	621	52.0	224	2	Q7SVQ4
18	619.5	51.9	219	2	Q8MUT9
19	619	51.8	221	2	Q95WZ7
20	618.5	51.8	235	2	Q9USA1
21	617.5	51.7	235	1	1CPX DIRIM
22	609.5	51.0	222	2	Q8GVJ5
23	607.5	50.9	224	2	Q8BG37
24	599	50.2	222	2	Q694A9
25	599	50.2	232	1	TSA_ONCVO
26	595.5	49.9	249	2	Q7QIQ4
27	588	49.2	222	2	Q9GPQ2
28	588	49.2	222	2	Q9VQI7
29	587	49.2	222	2	Q95SB0
30	575	48.2	216	2	Q9G5V3
31	572.5	47.9	219	2	Q9SP12

32 521.5 43.7 248 2 Q7PZB4
33 517.5 43.3 220 2 Q8GVH0
34 514.5 43.1 220 2 Q8GVG9
35 513.5 43.0 219 2 Q8S3K4
36 509 42.6 218 2 Q8E2Z6
37 508.5 42.6 220 1 REHY ORYSA
38 503 42.1 211 2 Q8DQ04
39 502.5 42.1 220 2 Q694A7
40 501.5 42.0 220 2 Q9GPQ1
41 501.5 42.0 220 2 Q9V5K7
42 501.5 42.0 231 2 Q8MYT1
43 500 41.9 218 2 Q6W8Q2
44 499 41.8 226 2 Q6BLY9
45 498.5 41.8 220 2 Q9GPQ0

ALIGNMENTS

RESULT 1

Q962X0 PRELIMINARY; PRT; 224 AA.
AC Q962X0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Peroxidoxin 2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Ding M., Soldati D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397213; AAK77610.1; -;
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR SEQUENCE 224 AA; 24462 MW; 16FIA05842DBED5C CRC64;

Query Match 59.2%; Score 707; DB 2; Length 224;
Best Local Similarity 57.0%; Pred. No. 4e-58;
Matches 136; Conservative 36; Mismatches 57; Indels 2; Gaps 1;
QY 3 LNLGDSFPDFOAEALG--AEHFLHEYLGDVGWGFMSHPNDPTVCTTELAELAVKLODSF 60
DB 2 LVLGSTFPDVAADAGVPGDKIKLYDFLGDVGWGLMSHPDFTPVCTTELAQAARMAPEF 61
QY 61 TKKNCKLVGFSCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKD 120
DB 62 AKRNCKLIGFSCDDVSSHKGWAKDVMSVAKLSGDLFPPIADPERKLTATDLGIMDPEEKD 121
QY 121 KKGFLPTCRVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDDWTA 180
DB 122 KAGIPVTCRAAIYIGDPRRVKGLILYPATVGRNFKVLRALDALQAEKYPVATPEGWFP 181
QY 181 GAKCCVVPNLAAEAEORLLPKGHEALQLPSGKPYLRLTPDP 221
DB 182 GDKVMVQPTLTDEAKAKLPKGFEKCEPSGKNYLYAPDP 222

RESULT 2

PDX6_RAT STANDARD; PRT; 223 AA.
AC Q35244;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peroxiredoxin 6 (EC 1.1.1.1.-) (Antioxidant protein 2) (1-Cys
DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
DE A2) (EC 3.1.1.-) (aiPLA2) (Non-selenium glutathione peroxidase)

DE (EC 1.11.1.7) (NSGPX) (Thiol-specific antioxidant protein).
GN Name=Prdx6; Synonyms=Alpa2, Aop2, Tsa;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RA Kim T.-S., Feinstein S.I., Dodia C., Hennigan B.B., Fisher A.B.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Olfactory epithelium;
RA Andreeva S.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 25-41 AND 145-162.
RX MEDLINE=97153037; PubMed=899971; DOI=10.1074/jbc.272.4.2542;
RA Kim T.-S., Sundaresh C.S., Feinstein S.I., Dodia C., Skach W.R.,
RA Jain M.K., Nagase T., Seki N., Ishikawa K.-I., Nomura N., Fisher A.B.;
RJ Biol. Chem. 272:10981-10981 (1997).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O(2) and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O(2) = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in
CC lung secretory organelles.
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
CC (to Cys-SO₃H) upon oxidative stress (By similarity).
CC -1- SIMILARITY: Belongs to the AhpC/TSA family. Redhydrin subfamily.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF014009; AAB6341.1; -;
DR EMBL; Y17295; CAA76732.1; -;
DR HSP; P30041; 1PRX.
DR RGD; 71005; Prdx6.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
KW Antioxidant; Direct protein sequencing; Hydrolase; Lipid degradation;
KW Lysosome; Multifunctional enzyme; Oxidoreductase; Peroxidase;
KW Redox-active center.
FT INIT MET 0 0 By similarity.
FT ACT_SITE 31 31 Phospholipase (By similarity).
FT ACT_SITE 46 46 Cysteine sulfenic acid (-SOH).
FT INTERMEDIATE (By similarity).
FT DISULFID 46 46 Interchain (in linked form) (By
FT similarity).
SQ SEQUENCE 223 AA; 24687 MW; B47E8537C975BF99 CRC64;
Query Match 56.08; Score 668.5; DB 1; Length 223;

Best Local Similarity 58.1%; Pred. No. 1.7e-54;
Matches 129; Conservative 29; Mismatches 59; Indels 5; Gaps 3;
QY 3 LNLGDSFPDQAE-ALGAERHRLHEYLGDGWSGVMFSDHNDFTPVCTTELAEAVKLQDSFT 61
DB 4 LLLGDEAPNFEANTIG--HIRFHDPLGDSWGLFSHPDRDFTPVCTTELGRAKLAPEFA 61
QY 62 KKNCKLVGFSNCDLQSHREWAKDIWYAGR--SGNLPFLVCDPNRELAAASLGIMDPAEK 119
DB 62 KKNVKLIALSIDSVDHFAWSKDINAYGAAPTEKLPFFIIDDKORDLAAILLGMLOPAEK 121
QY 120 DKKGPLTCTRCVFFISPEKKLAASILYPATTGNGFAEILRVLDLSLQLTAKFPVATPVDMT 179
DB 122 DEKGMPVTARVVVFIFGPDKKLSILYPATTGNGFDEILRVVDSLTASNPVATPVDMK 181
QY 180 AGAKCCVVPNLAAEEAQRLLPKGHEALQLPSPGKPYLRLTDPD 221
DB 182 KGESVMVLTPLPEEAKQLFPKGVFTKELPSGKKYLRYTPQ 223
RESULT 3
ID_PDX6_BOVIN STANDARD; PRT; 223 AA.
AC 077874;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peroxiredoxin 6 (BC 1.11.1.-) (Antioxidant protein 2) (1-Cys
DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
DE A2) (EC 3.1.1.-) (aPLA2) (Non-selenium glutathione peroxidase)
DE (EC 1.11.1.7) (NSGPX) (PHGPX) (Ciliary body glutathione peroxidase).
GN Name=PRDX6; Synonyms=AOP2, GPX, PHGPX;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ocular ciliary body;
RX MEDLINE=98421546; PubMed=9748299; DOI=10.1074/jbc.273.40.26171;
RA Singh A.K., Shichi H.;
RT "A novel glutathione peroxidase in bovine eye. Sequence analysis, mRNA
RT level, and translation."
RJ J. Biol. Chem. 273:26171-26178 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=99340074; PubMed=10409692; DOI=10.1074/jbc.274.30.21326;
RA Fisher A.B., Dodia C., Manevich Y., Chen J.-W., Feinstein S.I.;
RT "Phospholipid hydroperoxides are substrates for non-selenium
RT glutathione peroxidase."
RJ J. Biol. Chem. 274:21326-21334 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oviduct;
RA Rojas Garcia P.P., Einspanier R.;
RT "Glutathione peroxidase in the bovine oviduct."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-29.
RX MEDLINE=90323120; PubMed=2373154; DOI=10.1016/0014-4835(90)90040-2;
RA Shichi H., Demar J.C.;
RT "Non-selenium glutathione peroxidase without glutathione S-transferase
RT activity from bovine ciliary body."
RL Exp. Eye Res. 50:513-520 (1990).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O(2) and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O(2) = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in


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CC lung secretory organelles (By similarity).
CC -!- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
CC (to Cys-SO3H) upon oxidative stress (By similarity).
CC -!- SIMILARITY: Belongs to the AhpC/TSA family. Rehdyrin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF080228; AAC63016.1; -
CC EMBL; AF090194; AAC84043.1; -
CC EMBL; AJ243848; CAB64802.1; -
CC HSP; P30041; IPRX.
CC InterPro: IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC Redox-active center.
CC Lysosome; Multifunctional enzyme; Hydrolase; lipid degradation;
CC Redox-active center.
CC INIT MET 0 0 By similarity.
CC ACT_SITE 31 31 Phospholipase (By similarity).
CC FT ACT_SITE 46 46 Cysteine sulfinic acid (-SOH)
CC FT ACT_SITE 46 46 Intermediary (By similarity).
CC FT DISULFID 46 46 Interchain (in linked form) (By
CC similarity).
CC FT SEQUENCE 223 AA; 24935 MW; 4A2C89AC1E9A01E CRC64;

Query Match 54.6%; Score 652.5; DB 1; Length 223;
Best Local Similarity 56.8%; Pred. No. 5.3e-53;
Matches 126; Conservative 30; Mismatches 61; Indels 5; Gaps 3;

QY 3 LNLGDSFPDFOAE-ALGAEHFRLHEYLGDGSMGVFMSHPNDFTPVCTTTELAFAVKLQDSE 61
DB 4 LLLGDEAPNEANTTIG--RIRFHLYLGDGSMGLFSPHPRDFTPVCTTTELAGRAAKLAPEFA 61

QY 62 KKKCKLVGFCNDLQSHREWAKDIMAYAGR--SGNLPFPLVCDPNRELAASLGIMDPAEK 119
DB 62 KRNVMKIALSIDSVEDHLANSKDINAYNGEETKLPFPFIIDDKNRDLAIQLGMLDPAEK 121

QY 120 DKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATPDWT 179
DB 122 DEKGMPVTVARVVFIFGDPKKLSILYPATTGRNFDILRVISLQLTAEKRVATPDWK 181

QY 180 AGAKCCVVPNLAAEEAQRLLPKGHEALQLPSPKPYRLTDPD 221
DB 182 NGDSVMVLPTIPBEAAKKLPFGKGVFTKELPSGKKYLYTPQP 223

RESULT 4
Q9TSX9 PRELIMINARY; PRT; 224 AA.
ID Q9TSX9
AC Q9TSX9; 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Non-selenium glutathione phospholipid hydroperoxide peroxidase
DE (PHGPX).
GN Name=phgpx;
OS Sus scrofa (pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oviduct;

Query Match 53.9%; Score 644; DB 2; Length 220;
Best Local Similarity 56.7%; Pred. No. 3.3e-52;
Matches 123; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY 1 MPLNLGDSFPDFOAEALGAE-HPRLHEYLGDGSMGVFMSHPNDFTPVCTTTELAFAVKLQDS 59
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RA Rojas Garcia P.P., Einspanier R.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243849; CAB65456.1; -
DR HSP; P30041; IPRX.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR Peroxidase.
SQ SEQUENCE 224 AA; 25037 MW; D9929C7FDF51E77C CRC64;

Query Match 54.1%; Score 645.5; DB 2; Length 224;
Best Local Similarity 55.8%; Pred. No. 2.4e-52;
Matches 126; Conservative 32; Mismatches 61; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDFOAE-ALGAEHFRLHEYLGDGSMGVFMSHPNDFTPVCTTTELAFAVKLQ 57
DB 1 MPGLLLGDEAPNEANTTIG--RIRPHDPLGDSWGLFSPHPRDFTPVCTTTELAGRAAKLA 58

QY 58 DSFTKKNCKLVGFCNDLQSHREWAKDIMAYAGR--SGNLPFPLVCDPNRELAASLGIMD 115
DB 59 PEFAKRNVMKIALSIDSVEDHLANSKDINAYNGEETKLPFPFIIDDKNRDLAIQLGMLD 118

QY 116 PAEKOKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATP 175
DB 119 PAEKDEQGMPTVAVVFIFGDPKKLSILYPATTGRNFDILRVISLQLTAEKRVATP 178

QY 176 VDMTAGAKCCVVPNLAAEEAQRLLPKGHEALQLPSPKPYRLTDPD 221
DB 179 VDMKNGDSVMVLPTIPBEAAKKLPFGKGVFTKELPSGKKYLYTPQP 224

RESULT 5
Q7RGRI PRELIMINARY; PRT; 220 AA.
ID Q7RGRI
AC Q7RGRI; 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 1-cys peroxidoxin.
GN Name=PY04285;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNI;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; ABAL01001288; EAA16120.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 220 AA; 25293 MW; D1C8B370B7855D2F CRC64;

Query Match 53.9%; Score 644; DB 2; Length 220;
Best Local Similarity 56.7%; Pred. No. 3.3e-52;
Matches 123; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY 1 MPLNLGDSFPDFOAEALGAE-HPRLHEYLGDGSMGVFMSHPNDFTPVCTTTELAFAVKLQDS 59
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Db      1  MGVLGATPNFTAKASGIDGDFELYKIENSMAILFSPNDFTPVCTTTELAELGKHED 60
QY      60  FTKKNCKLVGFSNCLQSHREWAKOIMAYAGSGNLPFLVCDPNRELAASLGIMDPARK 119
Db      61  FLKLNCKLIGFSCNSKESHDKWIEDI-KYYGKLKWEIPIVCDSESLANKLKMDEQEK 119
QY      120  DKKGLPLTCRCVFFISPEKLAASILYPATTGNFAEILRVLDLSLQLTAKFPVATPDWT 179
Db      120  DITGLPLTCRCVFFISPEKIKATVLYPATTTGNAHEILRVLSLQLTYYTTPVATPVNWN 179
QY      180  AGAKCCVVPNLAEEAQRLLPKGHEALQPSGKPYLR 216
Db      180  EGDKCCVPIPLQDEISKHFKNBITKVMPSKKYLR 216

RESULT 6
Q86SB3  PRELIMINARY; PRT; 220 AA.
AC Q86SB3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1-Cys peroxidoredoxin.
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5861;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=17XL;
RX MEDLINE=22935300; PubMed=14572508; DOI=10.1016/S0020-7519(03)00184-X;
RA Kawazu S., Nozaki T., Tsuboi T., Nakano Y., Komaki-Yasuda K.,
RA Ikenoue N., Torii M., Kano S.;
RT "Expression profiles of peroxiredoxin proteins of the rodent malaria
RT parasite Plasmodium yoelii.";
RL Int. J. Parasitol. 33:1455-1461(2003).
DR EMBL; AB089300; BAC56716.1; -.
DR HSSP; P30041; IPRX.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 220 AA; 25293 MW; D1C9B370B7855D2F CRC64;

Query Match 53.9%; Score 644; DB 2; Length 220;
Best Local Similarity 56.7%; Pred. No. 3.3e-52;
Matches 123; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

QY      1  MPLNLGDSFPDFOAEALGAE-HFRLHEYLGDGSGVMFSPNDFTPVCTTTELAELGKHED 59
Db      1  MGVLGATPNFTAKASGIDGDFELYKIENSMAILFSPNDFTPVCTTTELAELGKHED 60
QY      60  FTKKNCKLVGFSNCLQSHREWAKOIMAYAGSGNLPFLVCDPNRELAASLGIMDPARK 119
Db      61  FLKLNCKLIGFSCNSKESHDKWIEDI-KYYGKLKWEIPIVCDSESLANKLKMDEQEK 119
QY      120  DKKGLPLTCRCVFFISPEKLAASILYPATTGNFAEILRVLDLSLQLTAKFPVATPDWT 179
Db      120  DITGLPLTCRCVFFISPEKIKATVLYPATTTGNAHEILRVLSLQLTYYTTPVATPVNWN 179
QY      180  AGAKCCVVPNLAEEAQRLLPKGHEALQPSGKPYLR 216
Db      180  EGDKCCVPIPLQDEISKHFKNBITKVMPSKKYLR 216

RESULT 7
Q6A0D0  PRELIMINARY; PRT; 227 AA.
AC Q6A0D0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA0106 protein (Fragment).
GN Names=MKIAA0106;
OS Mus musculus (Mouse).

Query Match 53.6%; Score 640.5; DB 2; Length 235;
Best Local Similarity 55.5%; Pred. No. 7.5e-52;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY      5  LGDSFPDFOAEALGAEHFLHEYLG-DSGVMFSPNDFTPVCTTTELAELGKHEDFTKK 63
Db      7  LGDKFPDFOAETSESPISFHDWIGKDSMAILFSPHPRDFTPVCTTTELAELVQLEPEFKR 66
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK172888; BAD32166.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR NON_TER 1
SQ SEQUENCE 227 AA; 25070 MW; CE3FFDB4A6280E17 CRC64;

Query Match 53.6%; Score 640.5; DB 2; Length 227;
Best Local Similarity 55.8%; Pred. No. 7.2e-52;
Matches 126; Conservative 27; Mismatches 66; Indels 7; Gaps 4;

QY      1  MP--LNLGDSFPDFOAE-ALGAEHFLHEYLGDGSGVMFSPNDFTPVCTTTELAELGKHED 57
Db      4  MFGLLLDGEAPNFANTTIG--RIRFHDFLGDGSGILFSPHPRDFTPVCTTTELGRAAKLA 61
QY      58  DSFTKKNCKLVGFSNCLQSHREWAKOIMAYAGR--SGNLPPFLVCDPNRELAASLGIMD 115
Db      62  PEFARKNVKLIALSIDSVEDHLAWSKIDINAYNGETPEKLPFIIDDKGRDLAILLGMLD 121
QY      116  PAKDKKGLPLTCRCVFFISPEKLAASILYPATTGNFAEILRVLDLSLQLTAKFPVATP 175
Db      122  PVEKDANNMPVTVRVVIFGPKLKLILYLPATTGNFAEILRVLDLSLQLTAKFPVATP 181
QY      176  VDWTAGAKCCVVPNLAEEAQRLLPKGHEALQPSGKPYLRITPDP 221
Db      182  VDWKKGESVMVVTLSSEBAKOCFPGVFTKELPSGKKYLRITPQP 227

RESULT 8
Q9U5A0  PRELIMINARY; PRT; 235 AA.
AC Q9U5A0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thiorodoxin peroxidase.
OS Brugia malayi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6279;
RN [1]
SEQUENCE FROM N.A.
RA Chandrasekar R., Tsuji N., Morales T., Carmody A., Ozols V.,
RA Welton J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF045165; AAF21098.1; -.
DR HSSP; P30041; IPRX.
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
DR Peroxidase.
KW Peroxidase.
SQ SEQUENCE 235 AA; 26223 MW; 41797A622217635C CRC64;

Query Match 53.6%; Score 640.5; DB 2; Length 235;
Best Local Similarity 55.5%; Pred. No. 7.5e-52;
Matches 127; Conservative 29; Mismatches 62; Indels 11; Gaps 3;

QY      5  LGDSFPDFOAEALGAEHFLHEYLG-DSGVMFSPNDFTPVCTTTELAELGKHEDFTKK 63
Db      7  LGDKFPDFOAETSESPISFHDWIGKDSMAILFSPHPRDFTPVCTTTELAELVQLEPEFKR 66
```

Qy 64 NCKLVGFSNDLQSHREWAKDIMAYGR-----SGN-LPPPLVCDPNRELAASLGI 113
 Db 67 NVKLGSLGSDVQSHRWADDIIELCRKSGDSNCTCCSGNKLPPFIADNRSLSKLG 126
 Qy 114 MDPRAKDKGLPLTRCVRFPISPKLAAILYPATTGRNFAELRLVDSLQLTAKPPVA 173
 Db 127 MDPDECDEKGAALTRCLFTIGPEKTKLSILYPATTGRNFDRLRVDSLQLTATKLVA 186
 Qy 174 TPVDWTAGAKCVCVVPNLAAEEAORLLPKGHEALQPSGKPYLRLTDPDR 222
 Db 187 TPVDWQNGDCVVPVTINDNEAKKLFGKINTVELPSGKPYLRVWAHPK 235

RESULT 9
 PDX6 MOUSE
 ID_PDX6_MOUSE STANDARD; PRT; 223 AA.
 AC 090709; Q9QWP4; Q9QW40;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
 DE Peroxiredoxin) (1-Cys PRX) (acidic calcium-independent phospholipase
 DE A2) (EC 3.1.1.-) (aPLA2) (Non-selenium glutathione peroxidase)
 DE (EC 1.11.1.7) (NSGpx).
 GN Name=Pdx6; Synonyms=Aop2, Ltw4, Prdx5;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
 RC STRAIN=C3H/FEJ, C57BL/6J, and DBA/2J; TISSUE=Kidney, and Liver;
 RX MEDLINE=97349116; PubMed=9205120; DOI=10.1006/geno.1997.4762;
 RA Iakubova O.A., Macella L.A., Her H., Beier D.R.;
 RT "Ltw4 protein on mouse chromosome 1 is a member of a family of
 RT antioxidant proteins";
 RL Genomics 42:474-478(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Skin;
 RX MEDLINE=97419117; PubMed=9291135;
 RA Munz B., Frank S., Huebner G., Olsen E., Werner S.;
 RT "A novel type of glutathione peroxidase: expression and regulation
 RT during wound repair";
 RL Biochem. J. 326:579-585(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain;
 RX MEDLINE=99326508; PubMed=10395907; DOI=10.1016/S0378-1119(99)00190-0;
 RA Lee T.-H., Yu S.-L., Kim S.-U., Kim Y.-M., Choi I., Kang S.W.,
 RA Rhee S.G., Yu D.-Y.;
 RT "Characterization of the murine gene encoding 1-Cys peroxiredoxin and
 RT identification of highly homologous genes";
 RL Gene 234:337-344(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balzarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varado R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Iehii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [5]
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 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain;
 RX MEDLINE=99326508; PubMed=10395907; DOI=10.1016/S0378-1119(99)00190-0;
 RA Lee T.-H., Yu S.-L., Kim S.-U., Kim Y.-M., Choi I., Kang S.W.,
 RA Rhee S.G., Yu D.-Y.;
 RT "Characterization of the murine gene encoding 1-Cys peroxiredoxin and
 RT identification of highly homologous genes";
 RL Gene 234:337-344(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pituitary;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,<

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DR EMBL; AF093855; AAD03716.1; JOINED.
DR EMBL; AF093856; AAD03716.1; JOINED.
DR EMBL; AK030413; BAC26952.1; -.
DR EMBL; BC013489; AAH13489.1; -.
DR HSSP; P30041; 1PRX.
DR SWISS-2DPAGE; O08709; MOUSE.
DR MGI; MGI:894320; Ptdx6.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
DR Antioxidant; Direct protein sequencing; Hydrolase; Lipid degradation;
KW Lysosome; Multifunctional enzyme; Oxidoreductase; Peroxidase;
FT INIT MET 0
FT ACT_SITE 31 31 Phospholipase (By similarity).
FT ACT_SITE 46 46 Cysteine sulfenic acid (-SOH)
FT DISULFID 46 46 Intermediate (By similarity).
FT VARIANT 123 123 Interchain (in linked form) (By
FT 6J and strain C57BL/6, strain C57BL/
FT CONFLICT 153 153 D -> A (in strain C57BL/6, strain C57BL/
FT CONFLICT 180 180 G -> S (in Ref. 3; AAC67553).
FT CONFLICT 180 180 W -> R (in Ref. 3; AAD03716).
SQ SEQUENCE 223 AA; 24739 MW; A4F2B1E36180BBFC CRC64;

Query Match 53.68; Score 639.5; DB 1; Length 223;
Best Local Similarity 55.94; Pred. No. 8.8e-52;
Matches 124; Conservative 27; Mismatches 66; Indels 5; Gaps 3;

QY 3 LNLGDSPPDQAE--ALGAEHFRLHEVLGDSWGMFSGHPNDFTVCCTELAEAVKLQDSPT 61
DB 4 LLLGDEAPNEANTTIG--RIRPHDFLGDSWGLFSPDRDFTVCCTELGRAKLAPEFA 61
QY 62 KXCKLVGFCNDLQSHREWAKDIMAYAGR--SGNLPFFLVCDPNRELAASGIMPDAEK 119
DB 62 KRNVLIALSIDSVEDHLAWSKDINAYNGETPEKLPFFPIIDKGRDLAILGLMDPEVK 121
QY 120 DKXGLPLTCRCVFISPEKLAASILYPATTGRNFAELRLVLSLQLTAKFPVATPDVMT 179
DB 122 DNNMPVTARVTFIFGPKLKLILYPATTGRNFOELRLVDSLQLTGKVPATPDVWK 191
QY 180 AGAKCCVFNLAEEAQRLLPKGHEALQLPSGKPYRLRLTDP 221
DB 182 KGESVMVPTLSSEAAQCFPKGVFTKELPSGKKYLYTQP 223

RESULT 10
PDX6 HUMAN
ID_PDX6 HUMAN STANDARD; PRT; 223 AA.
AC P30041; P32077;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peroxiredoxin 6 (EC 1.11.1.-) (Antioxidant protein 2) (1-Cys
DE peroxiredoxin) (1-Cys PRX) (Acidic calcium-independent phospholipase
DE A2) (EC 3.1.1.-) (aIPUA2) (Non-selenium glutathione peroxidase)
DE (EC 1.11.1.7) (NSGPx) (24 kDa protein) (Liver 2D page spot 40) (Red
DE blood cells page spot 12).
GN Name=PRDX6; Synonyms=AOP2, KIAA0106;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Kim T.-S., Sundaresh C.S., Feinstein S.I., Dodia C., Skach W.R.,
RA Jain M.K., Nagase T., Seki N., Ishikawa K.-I., Nomura N., Fisher A.B.;
RL J. Biol. Chem. 272:2542-2550(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RC MEDLINE=95308325; PubMed=7788527;
RA Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA Tabata S., Ishikawa K.-I., Kawabayashi Y., Kotani H., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. III.
RT The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:37-43(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97203272; PubMed=9050990; DOI=10.1038/sj.onc.1200905;
RA Frank S., Munz B., Werner S.;
RT "The human homologue of a bovine non-selenium glutathione peroxidase
RT is a novel keratinocyte growth factor-regulated gene.";
RL Oncogene 14:915-921(1997).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Fetal brain, and Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whaley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwold J., Schmutz J., Myers R.M.,
RA Buttrickfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-21.
RX TISSUE=Platelet;
RC MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RN Nat. Biotechnol. 21:566-569(2003).
RN [7]
RP PARTIAL SEQUENCE OF 1-14.
RX TISSUE=Liver;
RC MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tisot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
RN [8]
RP PARTIAL SEQUENCE OF 1-12.
RX TISSUE=Erythrocyte;
RC MEDLINE=94147970; PubMed=8313871;
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tisot J.-D., Appel R.D., Walter C.,
RA Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
RN [9]
RP ERRATUM.

```

RP CHARACTERIZATION, AND MUTAGENESIS.
RX MEDLINE=98165813; PubMed=9497358; DOI=10.1074/jbc.273.11.6303;
RA Kang S.W., Baines I.C., Rhee S.G.;
RT "Characterization of a mammalian peroxidoxin that contains one
RL conserved cysteine";
RN J. Biol. Chem. 273:6303-6311 (1998).
[10]
RP CHARACTERIZATION, AND MUTAGENESIS.
RX MEDLINE=20435792; PubMed=10893423; DOI=10.1074/jbc.M005073200;
RA Chen J.-W., Dodia C., Feinstein S.I., Jain M.K., Fisher A.B.;
RT "1-Cys peroxidoxin, a bifunctional enzyme with glutathione
RL peroxidase and phospholipase A2 activities";
RN J. Biol. Chem. 275:28421-28427 (2000).
[11]
RP OXIDATION OF CYS-46.
RX MEDLINE=22201787; PubMed=12059788; DOI=10.1042/BJ20020525;
RA Wagner E., Luche S., Penna L., Chevillet M., van Dorsselaer A.,
RL Leize-Wagner E., Rabilloud T.;
RT "A method for detection of overoxidation of cysteines: peroxidoxins
are oxidized in vivo at the active-site cysteine during oxidative
stress";
RN Biochem. J. 366:777-785 (2002).
[12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=98246415; PubMed=9587003;
RA Choi H.-J., Kang S.W., Yang C.-H., Rhee S.G., Ryu S.-E.;
RT "Crystal structure of a novel human peroxidase enzyme at 2.0-A
RL resolution";
RN Nat. Struct. Biol. 5:400-406 (1998).
CC -1- FUNCTION: Involved in redox regulation of the cell. Can reduce
CC H₂O₂ and short chain organic, fatty acid, and phospholipid
CC hydroperoxides. May play a role in the regulation of phospholipid
CC turnover as well as in protection against oxidative injury.
CC -1- CATALYTIC ACTIVITY: Donor + H₂O₂ = oxidized donor + 2 H₂O.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic, lysosomal and also found in
CC lung secretory organelles (By similarity).
CC -1- MISCELLANEOUS: The active site is the redox-active Cys-46 oxidized
CC to Cys-SOH. Cys-SOH may rapidly react with a Cys-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin.
CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-46
CC (to Cys-SO₃H) upon oxidative stress.
CC -1- SIMILARITY: Belongs to the AhpC/TSA family. Rehydrin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC ENBL; D14662; BAA03496.1; --
CC ENBL; BC035857; AAH35857.1; --
CC ENBL; BC035550; AAH35550.1; --
CC PDB; 1PRX; X-ray; A/B=1-223.
CC SWISS-2DPAGE; P30041; HUMAN.
CC OGP; P30041; --
CC Sienna-2DPAGE; P30041; --
CC Genew; HGNC:16753; PRDX6.
CC H-InvdB; HIX0001339; --
CC MIM; 602316; --
CC GO; GO:0005829; C:cytosol; NAS.
CC GO; GO:0016209; F:antioxidant activity; NAS.
CC GO; GO:0016224; F:non-selenium glutathione peroxidase activity; IDA.
CC GO; GO:0004623; F:phospholipase A2 activity; IDA.
CC GO; GO:0009395; P:phospholipid catabolism; IDA.
CC GO; GO:0006979; P:response to oxidative stress; IDA.
CC InterPro; IPR000866; AhpC-TSA.
CC Pfam; PF00578; AhpC-TSA; 1.
CC 3D-structure; Antioxidant; Direct protein sequencing; Hydrolase;
KW

KW Lipid degradation; Lysosome; Multifunctional enzyme; Oxidoreductase;
KW Peroxidase; Redox-active center.
FT INIT_MET 0 0 Phospholipase.
FT ACT_SITE 31 31 Cysteine sulfenic acid (-SOH)
FT ACT_SITE 46 46 Intermediate.
FT DISULFID 46 46 Interchain (in linked form) (By
FT similarity).
FT MUTAGEN 31 31 S->A: Loss of AIPLA2 activity, but no
FT effect on NSGFX activity.
FT MUTAGEN 46 46 C->S: Loss of NSGFX activity, but no
FT effect on AIPLA2 activity.
FT TURN 6 7
FT STRAND 9 9
FT STRAND 14 17
FT TURN 18 19
FT STRAND 20 23
FT HELIX 24 28
FT TURN 29 30
FT STRAND 32 38
FT HELIX 44 61
FT TURN 62 64
FT STRAND 65 71
FT HELIX 75 88
FT TURN 89 90
FT STRAND 101 103
FT TURN 105 106
FT HELIX 108 112
Query Match 53.4%; Score 637.5; DB 1; Length 223;
Best Local Similarity 56.6%; Pred. No. 1.4e-51;
Matches 125; Conservative 28; Mismatches 65; Indels 3; Gaps 2;
Qy 3 LNLGDSFPQAEALGAERHLEHLYGLDGSWGVFNSHPNDFTPVCTTELAEAVKLQDSFTK 62
Db 4 LLLGDVAPNEANTT-VGRIRHDFLDGSGWILFSPDRDFTPVCTTELGRAAKLAPEFAK 62
Qy 63 KNCJLVGFCNDLQSHREWAKOIMAY--AGRSNLPFPLVCDPNRELAASLGIMDPAEKD 120
Db 63 RNVKLTALSIDSVEDHLAWSKOINAYNCEPTEKLPFPIDDRRELAILLGMGLDPAEKD 122
Qy 121 KGLPLTCTRCVFFISPEKKLAASILYPATTGRNFAEILRVLSLQLTAKPPVATPVDMTA 180
Db 123 EKGMPVTARVVFVFGDPKKLSILYPATTGRNFDILRVVISLQLTAEKRVRATPVDMKD 182
Qy 181 GAKCCVVPNLAAEAERLLPKGHEALQLPSGKDYRLTPDP 221
Db 183 GDSVMVLTPIPEBEAKLPKGVFTKELPSGKKLYRTPDP 223
RESULT 11
Q8IAM2 PRELIMINARY; PRT; 220 AA.
ID Q8IAM2 PRELIMINARY; PRT; 220 AA.
AC Q8IAM2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-cys peroxidoxin.
GN Names:1-cyspxn; Synonyms:PF08_0131;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL844507; CAD51341.1; --
DR HSSP; P30041; 1PRX
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.
SQ SEQUENCE 220 AA; 25164 MW; ECDA692845B8A15F CRC64;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Klein S., Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC054278; AAH54278.1; -.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 SQ SEQUENCE 224 AA; 25363 MW; 7CD67F59315A3CAB CRC64;
 Query Match 52.6%; Score 628; DB 2; Length 224;
 Best Local Similarity 53.1%; Pred. No. 1.1e-50;
 Matches 120; Conservative 37; Mismatches 63; Indels 6; Gaps 4;
 QY 1 MP-LNLGDSPPDQAE-ALGAEHRLHEYLGDGSGWVMSHPNDFTPVCTTELAEAVKLQD 58
 Db 1 MPGLIGLRRPDEADTTIG--RIKFHFPIGRWGLVFSHPDRTPVCTTELGRCVKLAP 58
 QY 59 SFTKKNCKLVGFCNDLQSHREWAKDITMAY--AGRSNLPFPLVCDPNRELAASLGIMDP 116
 Db 59 EFKRNVRMTALSDSVDHLGSKDINSYNCDEPTETLEFPPIADPKDLAVQLGMLDP 118
 QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPV 176
 Db 119 DEKDMQMPVPTVPEEARKIFTCGVFTKELPSGKKYLYTTPQ 224
 QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDPDR 222
 Db 179 DWKPGDRVMVPTVPEEARKIFTCGVFTKELPSGKKYLYTTPQ 224
 RESULT 15
 Q966Y9
 ID Q966Y9 PRELIMINARY; PRT; 217 AA.
 AC Q966Y9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glutathione peroxidase.
 GN Name-gpx;
 OS Suberites domuncula (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Hadromerida; Suberitidae; Suberites.
 OX NCBI_TaxID=55567;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20033590; PubMed=10564648;
 RA Kruse M., Steffen R., Batel R., Mueller I.M., Mueller W.E.G.;
 RA "Differential expression of allogaft inflammatory factor 1 and of
 RT glutathione peroxidase during auto- and allograft response in marine
 RT sponges.";
 RL J. Cell. Sci. 112:4305-4313(1999).
 DR EMBL; Y18438; CAC38779.1; -.
 DR HSSP; P30041; IPRX.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Peroxidase.
 SQ SEQUENCE 217 AA; 24131 MW; 924PAC1550F63B0B CRC64;
 Query Match 52.4%; Score 625.5; DB 2; Length 217;
 Best Local Similarity 52.3%; Pred. No. 1.7e-50;
 Matches 116; Conservative 38; Mismatches 63; Indels 5; Gaps 4;
 QY 1 MELNLGDSPPDQAEALGAEHRLHEYLGDGSGWVMSHPNDFTPVCTTELAEAVKLQDSF 60
 Db 1 MP-LNQQIFPNFEADTTEGP-IKFHDWLGDMGILFHPADFTPVCTTELTGTVAKLVPEF 58
 QY 61 TKKNCKLVGFCNDLQSHREWAKDITMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEKD 120
 Db 59 QQRNVKVIASCDPVDSHKTWKIDIESY-GKLUSSFGYPIIADKNRELAQVQFGLMDPEEKD 117
 QY 121 KKGPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLSLQLTAKFPVATPVDMTA 180
 Db 118 KAGLPLTARAVFIIGPKLKLKSLLYPATTGRNFDEILRVDSLQLTAYKKVATPANWKN 177
 QY 181 GAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDPDR 222
 Db 178 GSKCMILPSVSKDEAKF--PGVETADVPSSGKKYIRLADQPK 217
 RESULT 16
 Q6P624
 ID Q6P624 PRELIMINARY; PRT; 224 AA.
 AC Q6P624;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC76137.
 GN Name=MGC76137;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RP	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUB=Embryo;	
RL	Klein S., Gerhard D.S.;	
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.	
DR	EWBL; BC062510; AAH62510.1, --	
KW	Hypothetical protein.	
QY	SEQUENCE 224 AA; 25156 MW; 5C4813E444AF7AB CRC64;	
Query Match 52.0%; Score 621; DB 2; Length 224;		
Best Local Similarity 54.0%; Pred. No. 4.8e-50;		
Matches 122; Conservative 33; Mismatches 65; Indels 6; Gaps 4;		
Qy	1 MP-INLGDSPDFOAE-ALGAEHRLHLYLGDSGVMFSPNDPTFVCTTELAAVAKLQD 58	
	: : : : : : :	
Db	1 MPGLLLGEIFPDFEADTTIG--RIKHFELGSGWGLFSPHDPVTPVCTTELGRVCVKLAP 58	
	: : : : : : :	
Qy	59 SFTKKNCKLVGFSCLDQSHREWAKDIMAY--AGRSGNLPEPLVCDPNRELAASIGIMDP 116	
	: : : : : : :	
Db	59 EFKRNVRMIALSIDSVEDHLGWSKDSYNSNCDEFTFLPFPIIADPKRDVAVLGMLQD 118	
	: : : : : : :	
Qy	117 AEKDKGLPLTRCQVFFISPEKLAASILYPATTTGRNFAETLRVLDSLQLTAKPVPATPV 176	
	: : : : : : :	
Db	119 DEKDMQMPVTARCFFIIGPKKMLSLIYPATTTGRNFEDELRVVDLSQLTAVHNATPV 178	
	: : : : : : :	
Qy	177 DWTAGAKCCVVPVNAASEAQRLLPKGHALQLPSGKPYLRITPPDR 222	
	: : : : : : :	
Db	179 DWKPGDRVVPVNPVPEBEASKLPSGVFNKALPSRKNYLRVTAHPQ 224	
	: : : : : : :	
RESULT 17		
Q7SYQ4	PRELIMINARY; PRT; 224 AA.	
AC	Q7SYQ4;	
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	MG664582 protein.	
GN	Name=MG664582;	
OS	Xenopus laevis (African clawed frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC	Xenopodidae; Xenopus.	
OX	NCBI_TaxID=8355;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUB=Whole;	
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshitsuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	

RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUB=Whole;
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative." Dev. Dyn. 225:384-391(2002).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUB=Whole;
RA	Klein S., Strausberg R.; Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC054309; AAH54309.1; -
DR	InterPro: IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
SQ	SEQUENCE 224 AA; 25070 MW; BDBEBE6013ECNA5A CRC64;
Query Match	52.0%; Score 621; DB 2; Length 224;
Best Local Similarity	53.1%; Pred. No. 4.8e-50;
Matches 120; Conservative	36; Mismatches 64; Indels 6; Gaps
Qy	1 MP-LNLGDSPPDFOAE--ALGAEHFRLLHYLGDSKGMFSEHPNDFFPVCTTELAEAVKLOD 58 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Dd	1 MPGILLGDVFPNFADTTIG--RIKFHDFLGNSWGVLEFSHPRDYTPVCETELGRVCVKLAP 58 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Qy	59 SFTKNCKLVGFSCNDLQSHREWAQDKIMAY--AGRSGNLPPLVCDPNRELAASLGIMDP 116 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Dd	59 EFKRNVSMIALSDSVEDHLGNSKDINSYNCEDETFETLPPIIADPKRELAVQLGLMDP 118 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Qy	117 AEKDKGLPLTRCVRFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVPATPV 176 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Dd	119 DEKDMQMPVTARCVFIIIGPKMKLSILYPATTGRNFDEILRVVDLSQLTAVHNVPATPV 178 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Qy	177 DWTAGAKCCVVVNAAEEAQRLLPKGHEALQLPSGKPYLRUTPDPR 222 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
Dd	179 DWKPGDRVVMVPPNPVEEASKIFTGCVFTKELPSGKYLRVTAQPQ 224 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::
RESULT 18	
Q8MUT9	PRELIMINARY; PRT; 219 AA.
ID	Q8MUT9
AC	Q8MUT9;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Glutathione peroxidase.
OS	Aplysia californica (California sea hare).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC	Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidae;
OC	Aplysioidae; Aplysiidae; Aplysia.
NCBI_taxid=6500;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Panchin Y.V., Bodnarova M., Moroz L.L.; Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF510851; AAA44290.1; -
DR	HSPF; P30041; 1PRX.
GO	GO:0004601; F:peroxidase activity; IEA.
DR	InterPro: IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
SQ	SEQUENCE 219 AA; 24167 MW; 77ED48CAAB3565B5 CRC64;
Query Match	51.9%; Score 619.5; DB 2; Length 219;
Best Local Similarity	54.1%; Pred. No. 6.5e-50;
Matches 118; Conservative	33; Mismatches 64; Indels 3; Gaps

Qy 3 LNLGDSFPDFOAALGAHFRHLHYLGDSWGMFMSHPNDFTPVCTTBLAABAVKLQDSFTK 62
 Db 2 VNLGDVPFNFTANTSKGE- IKFHDWLGSMALLFSHPADYTPVCTTBLARVVTLLAPEFEK 60
 Qy 63 KNCVLGFSNDLQSHREAWKDIMAYA-GRSGNLPFLVCDPNRELAASLGIMDPAEKDK 121
 Db 61 RGVKLIALSCDGVNSHVGWGDVNTFAGQKDDLPYPIVADDEERKLAELGMDIPDERTK 120
 Qy 122 KGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPDVWTAG 181
 Db 121 EGLPLTARAVPIIGDKKLKLUSLYPATTTGRNFNGILRVDSLQLTATQKVTATPDVWEKG 180
 Qy 182 AKCCVVPNLAABEAAQRLLPKGHEALQLPSPGKPYLRLLTP 219
 Db 181 QKCMVLPITPMDAERKLPF-NMEVRDVPSEGBYLRFPT 217

RESULT 19
 Q95WZ7
 ID Q95WZ7 PRELIMINARY; PRT; 221 AA.
 AC Q95WZ7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glutathione peroxidase.
 GN Name=gph;
 OS Ixodes scapularis (Black-legged tick) (Deer tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
 OX NCBI_TaxID=6945;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Das S., Banerjee G., DePonte K., Marcantonio N., Kantor F.S.,
 RA Fikrig E.;
 RT "Salp5d, an Ixodes scapularis antioxidant, is one of 14
 RT immunomodulant antigens in engorged tick salivary glands.";
 RL J. Infect. Dis. 184:0-0(2001).
 DR EMBL; AF209911; AAK97814.1; -.
 DR HSSP; P30041; 1PRX.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 KW Peroxidase.
 SQ SEQUENCE 221 AA; 24566 MW; AB287CD3F3B34B50 CRC64;

Query Match 51.8%; Score 619; DB 2; Length 221;
 Best Local Similarity 51.8%; Pred. No. 7.3e-50;
 Matches 114; Conservative 35; Mismatches 69; Indels 2; Gaps 2;

Qy 2 PLNLGDSFPDFOAALGAHFRHLHYLGDSWGMFMSHPNDFTPVCTTBLAABAVKLQDSFT 61
 Db 3 PLNLGDSFPNFTCDTTGK-IDFHEWLGNSWGLFSPADYTPVCTSELARAAQLHHVFQ 61
 Qy 62 KNCVLGFSNDLQSHREAWKDIMAYAG-RSGNLPFLVCDPNRELAASLGIMDPAEKD 120
 Db 62 KKGVLIALSCDSVESHRGMIKIDINAFGELPDGPPYPIADEKRDIAVKGMLDPVEKD 121
 Qy 121 KGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPDVWTAG 180
 Db 122 KEGPLTCRAVFIIGDKKLKLUSLYPATTTGRNFNGILRVDSLQLTATQKVTATPDVWEKG 181
 Qy 181 GAKCCVVPNLAABEAAQRLLPKGHEALQLPSPGKPYLRLLTPD 220
 Db 182 GTPCWLVPSTVEEILKLFPTGIKQYEVPSGKNYLRITMD 221

RESULT 20
 Q9U5A1
 ID Q9U5A1 PRELIMINARY; PRT; 235 AA.
 AC Q9U5A1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Thioexodxin peroxidase.
 OS Dirofilaria immitis (Canine heartworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Dirofilaria.
 OX NCBI_TaxID=6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20189524; PubMed=10726990;
 RA Chandrashekar R., Tsuji N., Morales T.H., Carmody A.B., Ozols V.O.,
 RA Welton J., Tang L.;
 RT "Removal of hydrogen peroxide by a l-cysteine peroxidexodxin enzyme of
 RT the filarial parasite Dirofilaria immitis.";
 RL Parasitol. Res. 86:200-206(2000).
 DR EMBL; AF045164; AAF21097.1; -.
 DR HSSP; P30041; 1PRX.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 KW Peroxidase.
 SQ SEQUENCE 235 AA; 26298 MW; D177468FA6B47576 CRC64;

Query Match 51.8%; Score 618.5; DB 2; Length 235;
 Best Local Similarity 54.1%; Pred. No. 8.8e-50;
 Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;

Qy 5 LGDSFPDFOAALGAHFRHLHYLG-DSWGMFMSHPNDFTPVCTTBLAABAVKLQDSFTK 63
 Db 7 LGDKFPDFRAETWEGFIPSYDWIGKDSMAILFSHPRDFTPVCTTBLARVVLQALPEPKR 66
 Qy 64 NCKLVGFSNDLQSHREAWKDIMAYAGR-----SGN-LPFPVLVCDPNRELAASLGI 113
 Db 67 NVKLIGLSCDSAESHRKVVDDINAVCKMKCNDGDTCCSGNKLFPPIADENRFLATELGM 126
 Qy 114 MDAPEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVPA 173
 Db 127 MDPDERDENGALTCRVFIIGPEKTLKLSILYPATTGRNFDLRLVDSLQLTAVKLVA 186
 Qy 174 TPVDWTAGKCCVVPNLAABEAAQRLLPKGHEALQLPSPGKPYLRLLTPDPR 222
 Db 187 TPVDWKGDDCVLPTIDTTEAKKLGKEINTIEFSGHLYRWVAHPK 235

RESULT 21
 1CPX DIRIM
 ID 1CPX DIRIM STANDARD; PRT; 235 AA.
 AC Q17433;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 1-Cys peroxidoxin (EC 1.11.1.7) (1-CysPxn).
 OS Dirofilaria immitis (Canine heartworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Dirofilaria.
 OX NCBI_TaxID=6287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McConigle S., James E.R.;
 RT "1-Cys peroxidoxin from Dirofilaria immitis.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Thiol specific antioxidant.
 CC -1- CATALYTIC ACTIVITY: Donor + H(2)O(2) = oxidized donor + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: Cys-49 is the site of oxidation by H(2)O(2). The oxidized
 CC intermediate might be Cys-SOH (By similarity).
 CC -1- SIMILARITY: Belongs to the ahpC/TSA family. Redhydrin subfamily.
 CC -----
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RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki R., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK029613; BAC26531.1; -;
DR ENBL; AK077012; BAC36564.1; -;
DR HSSP; P30041; IPRX.
DR MGD; MGI:131688; Prdx6-rel.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 224 AA; 24996 MW; CC30869EA99026 CRC64;
Query Match 50.9%; Score 607.5; DB 2; Length 224;
Best Local Similarity 52.7%; Pred. No. 8.9e-49;
Matches 119; Conservative 32; Mismatches 68; Indels 7; Gaps 4;
QY 1 MP--LNLGDSFPDFQAE-ALGAHFRLHEYLGDGSGVMFSPNDFTPVCTTLEAAVQLQ 57
DB 1 MPGLLIGAEAPDFEANTTIG--RIRPHDFLNGSMGLFSPKDFTPVCTTLEGRAAKLA 58
QY 58 DSTTKNCKLVGSCNDLQSHREWAKDIMAYAGRS--GNLPFLVCDPNRELAASLGIMD 115
DB 59 PEFKRNKVLIALSVDSVEDHLAWSKDINAYNGATPKELPFPIIDDKDRDISILFCMLD 118
QY 116 PAEKDKKGLPLTCRCVFFISPEKLAASILYPATTGNFPAEILRLVDSLQLTAKFPVATP 175
DB 119 PVEKDANSMLTARGVIFGFDKLLKMSLLYPNSTGRNFDILRLVDSLQLTETKPVATP 178
QY 176 VDWTAGKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYLRLTPDP 221
DB 179 VDWKKGESVWVLPDLPEEAACRFPKGIISTTKLPSPGKNLYRYTPQP 224
RESULT 24
Q694A9 PRELIMINARY; PRT; 222 AA.
AC Q694A9
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Putative peroxiredoxin.
OS Glossina morsitans morsitans.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Hippoboscidae; Glossinidae; Glossina.
OX NCBI_TaxID=37546;
RN [1]
RP SEQUENCE FROM N.A.
RA Munks R.J.L., Grail W., Igglesden T.J., Lehane M.J.;
RT "Antioxidant genes from the Tsetse fly Glossina morsitans morsitans."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY625503; AAT85820.1; -;

DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 222 AA; 25002 MW; 0A228CC383CB4526 CRC64;
Query Match 50.2%; Score 599; DB 2; Length 222;
Best Local Similarity 49.5%; Pred. No. 5.5e-48;
Matches 110; Conservative 38; Mismatches 66; Indels 8; Gaps 3;
QY 3 LNLGDSFPDFQAEALGAHFRLHEYLGDGSGVMFSPNDFTPVCTTLEAAVQLQDSFTK 62
DB 6 LNLGDSFPDFQAEALGAHFRLHEYLGDGSGVMFSPNDFTPVCTTLEAAVQLQDSFTK 64
QY 63 KCKLVGSCNDLQSHREWAKDIMAYAGRSNLP---FPLVCDPNRELAASLGIMDPAEK 119
DB 65 RKVKPIALSCDTVETHTKGIWEDISKY---GKLPXVDYPIIGDKERKLAVKLMLDKDEI 120
QY 120 KKKGLPLTCRCVFFISPEKLAASILYPATTGNFPAEILRLVDSLQLTAKFPVATPVDWT 179
DB 121 NAEGLPMT CRAVFIVDESCKLRQLIYPATTGNFPAEILRLVDSLQLTAKFPVATPVDWT 180
QY 180 AGAKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYLRLTPDP 221
DB 181 QGETCMILPTVSDXASRKYPKGFKTINVPSPGKPYMRQTPQP 222
RESULT 25
TSA ONCVO STANDARD; PRT; 232 AA.
AC P52570;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thiol-specific antioxidant.
GN Name-TSA;
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Chandrasekar R., Curits K.C., Weil G.J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-222 FROM N.A.
RA Chandrasekar R., Curits K., Weil G.J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ahpc/TSA family. Renydrin subfamily.
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CC
CC EMBL; U31052; AAC27392.1; -;
CC EMBL; U09385; AAS50214.2; -;
CC HSSP; P30041; IPRX.
CC InterPro; IPR000866; Ahpc-TSA.
CC Pfam; PF00578; Ahpc-TSA; 1.
CC Antioxidant.
FT ACT SITE 49 49 By similarity.
SQ SEQUENCE 232 AA; 25925 MW; 029E93F276232B37 CRC64;
Query Match 50.2%; Score 599; DB 1; Length 232;
Best Local Similarity 51.5%; Pred. No. 5.9e-48;
Matches 118; Conservative 30; Mismatches 73; Indels 8; Gaps 2;
QY 2 PLNLGDSFPDFQAEALGAHFRLHEYLGDGSGVMFSPNDFTPVCTTLEAAVQLQDSF 60
DB 4 PPSGPNKFPDFQAEALGAHFRLHEYLGDGSGVMFSPNDFTPVCTTLEAAVQLQDSF 63

QY 61 TKKNCKLVGFSNDLQSHREWAKDIMAY-----AGRSNLPFPPLVCDPNRELAASLGI 113
 DB 64 KKRNVKLJGLSCDSADSHSKWADIIALYRMKCVGCDSEKKLPFYPIIADDESLATELGM 123
 QY 114 MPAEKDKKGLPLTCRCVFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVA 173
 DB 124 MPDERDEKGNLTARCVIIGSDKTLKLSILYPATTGRNFAELRLVDSLOLTAVKLV 183
 QY 174 TPVDMTAGKCCVVPNLAABEQRLLPKGHEALQPLSGKPYRLTDPDR 222
 DB 184 TPVDMKGDGCVLPITDIDNEAKKLFGEKHTITDLPFGKHLYRMVPHK 232
 RESULT 26
 Q7QIQ4 PRELIMINARY; PRT; 249 AA.
 AC Q7QIQ4; (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DE AGCP3392 (Fragment)
 GN Name=agCG54406; ORFNames=ENSGANG00000012627;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB01008807; EAA04146.1; --
 DR InterPro: IPR000866; AhpC-TSA.
 DR Pfam: PF00578; AhpC-TSA; 1.
 FT NON_TER 1
 SQ SEQUENCE 249 AA; 27277 MW; 8D3591162B8832DE CRC64;

Query Match 49.9%; Score 595.5; DB 2; Length 249;
 Best Local Similarity 52.7%; Pred. No. 1.4e-47;
 Matches 118; Conservative 28; Mismatches 73; Indels 5; Gaps 3;
 QY 1 MPLNLGDSFPDFOAE-ALGAHFRHLHEYLGDGSGVMFHPNDFTPVCTTTELAEAVKLQDS 59
 DB 27 MSLNLGDPFNFATDTTIGDIFD--HQWIGDGWAILFHPADYTPVCTTTELAAVAKLVE 84
 QY 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYA--GRSGNLPFPPLVCDPNRELAASLGIMDPA 117
 DB 85 FTKRNYKPTALSCTVESHGRGWIEDIKAYGQLAAADPPFPPIIDDSKRELAVKLNMLDRD 144
 QY 118 EKDKKGLPLTCRCVFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATPVD 177
 DB 145 EIGSAGLPLTCRAVFDVIGDKKRLSLILYPATTGRNFAELRLVDSLOLTAKFPVATPVD 204
 QY 178 WTAGAKCCVVPNLAABEQRLLPKGHEALQPLSGKPYRLTDPDR 221
 DB 205 WMPGDSQWQPTVPADQLATLFPAGVDSVTLPSGKQYLKRTCEP 248

RESULT 27
 Q9GQP2 PRELIMINARY; PRT; 222 AA.
 AC Q9GQP2; (T-EMBLrel. 16, Created)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
 DE 1-cys peroxiredoxin DFX-6005.
 GN Name=Prx6005;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21534478; PubMed=11677042; DOI=10.1016/S0891-5849(01)00692-X;
 RA Radvuk S.N., Klitchko V.I., Spinola B., Sohal R.S., Orr W.C.;
 RT "The peroxiredoxin gene family in Drosophila melanogaster.";
 RL Free Radic. Biol. Med. 31:1090-1100(2001).
 DR EMBL: AF3111878; AAG47822.1; --
 DR HSSP: P30041; 1PRX.
 DR FLYBase: FBgn0031479; Prx6005.
 DR InterPro: IPR000866; AhpC-TSA.
 DR Pfam: PF00578; AhpC-TSA; 1.
 SQ SEQUENCE 222 AA; 24841 MW; 6FBA23BEBDA66318 CRC64;
 Query Match 49.2%; Score 588; DB 2; Length 222;
 Best Local Similarity 49.3%; Pred. No. 6e-47;
 Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;
 QY 3 LNLGDSFPDFOAEALGAHFRHLHEYLGDGSGVMFHPNDFTPVCTTTELAEAVKLQDSFTK 62
 DB 6 LNLGQDPFNFATET-SEGRIDFYDMQDSWAILFHPADFTPVCTTTELSRVAALIPFQK 64
 QY 63 KNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKDKK 122
 DB 65 RVGKPTALSCTVESHGRGWIEDIKSF-GKLSGDFYPIIADDESLATELGMKLNMLDKDINAE 123
 QY 123 GLPLTCRCVFFISPEKLAASILYPATTGRNFAELRLVDSLOLTAKFPVATPVDWTAGA 182
 DB 124 GIPLTCRAVFDVIGDKKRLSLILYPATTGRNFAELRLVDSLOLTAKFPVATPVDWTAGA 183
 QY 183 KCVVPNLAABEQRLLPKGHEALQPLSGKPYRLTDPDR 221
 DB 184 KCVLPFTVKAEDVPKFLPDGDIETIELPSGKSYLRITPQP 222
 RESULT 28
 Q9VQI7 PRELIMINARY; PRT; 222 AA.
 AC Q9VQI7; (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE CG3083-PA.
 GN Name=Prx6005; ORFNames=CG3083;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 OX NCBI_TaxID=3880;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Boudet J., Buitink J., Satour P., Leprince O.H.L.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AY594329; AAT67997.1; --
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 SQ SEQUENCE 218 AA; 24414 MW; B6C138B69F698CE4 CRC64;

Query Match 42.6%; Score 509; DB 2; Length 218;
 Best Local Similarity 42.5%; Pred. No. 1.5e-39;
 Matches 93; Conservative 44; Mismatches 78; Indels 4; Gaps 4;

QY 1 MP-LNLGDSPPDQAEALGAHEHRLHEYLGDSDGVMFNSHPNDFTPVCTTTELAEAVALQDS 59
 DB 1 MPGLTIGDTVPNLELDSTHGK-IRIHDVGDTVVILFSGPDFTPVCTTTELAAMAAYAKE 59
 QY 60 FTKKNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEK 119
 DB 60 FNKRGVMLGMSCDLSEKHEWIKIEAHT-PGAKVNYPIISDPKREIIKQLNNVDPDEK 118
 QY 120 DKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWT 179
 DB 119 DSNQ-NLPSRALHIVGDPDKKILUSFLYPAQTGRNMDVLRVVSQKASKYKIATPANWK 177
 QY 180 AGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYRLT 218
 DB 178 PGEPVVISPDVTNDQAKEMFPQGFKTADLPKSKYLRFT 216

RESULT 37

REHY ORYZA
 ID REHY ORYZA STANDARD; PRT; 220 AA.
 AC P52573;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RAB24 protein.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica / Yuhkara;
 RA Fujino K., Tanaka K., Xu Z., Kikuta Y.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- INDUCTION: By abscisic acid (ABA).
 CC -1- SIMILARITY: Belongs to the ahpC/TSA family. Rehydrin subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR ENBL; D63917; BAA09947.1; --
 DR PIR; T03967; T03967.
 DR HSSP; P30041; IPRX.
 DR Gramene; P52573; --
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 KW Antioxidant.
 FT ACT_SITE 46
 SQ SEQUENCE 220 AA; 24142 MW; FIA522F6827133F9 CRC64;
 By similarity.

Query Match 42.6%; Score 508.5; DB 1; Length 220;
 Best Local Similarity 43.6%; Pred. No. 1.7e-39;

Matches 96; Conservative 46; Mismatches 73; Indels 5; Gaps 4;
 QY 1 MP-LNLGDSPPDQAEALGAHEHRLHEYLGDSDGVMFNSHPNDFTPVCTTTELAEAVALQDS 59
 DB 1 MPGLTIGDTVPNLELDSTHGK-IRIHDVGDTVVILFSGPDFTPVCTTTELAAMAAYAKE 59
 QY 60 FTKKNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEK 118
 DB 60 FDKRGVKKLGISCDVQSHKDFKIEAY--KPGNRVITYPIMADPSREAIKQLNNVDPDE 117
 QY 119 KKKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWT 178
 DB 118 KDSNGHLPRLAHIVGDPDKKILUSFLYPAQTCGRNMDVLRVVSQKASKYKIATPANWK 177
 QY 179 TAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYRLT 218
 DB 178 KGEPEVVISPDVTNDQAKEMFPQGFKTADLPKSKYLRFT 217

RESULT 38

QBDGQ4
 ID QBDGQ4 PRELIMINARY; PRT; 211 AA.
 AC Q8DQ04;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE AhpC/TSA family protein.
 GN OrderedLocustNames=tlr2261;
 OS Synecococcus elongatus (Thermosynechococcus elongatus).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=32046;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bp-1;
 RX MEDLINE=2225144; PubMed=12240834;

RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
 RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the thermophilic cyanobacterium
 RT Thermosynechococcus elongatus Bp-1";
 RL DNA Res. 9:123-130(2002).
 DR ENBL; AF005376; BAC09813.1; --
 DR HSSP; P30041; IPRX.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 KW Complete proteome.
 SQ SEQUENCE 211 AA; 23861 MW; 6FB5E8913545A16F CRC64;

Query Match 42.1%; Score 503; DB 2; Length 211;
 Best Local Similarity 45.5%; Pred. No. 5.4e-39;
 Matches 101; Conservative 44; Mismatches 63; Indels 14; Gaps 5;

QY 1 MPLNLGDSPPDF-QAEALGAHEHRLHEYLGDSDGVMFNSHPNDFTPVCTTTELAEAVALQDS 59
 DB 1 MSUKGVVVPNTQASSMGNIINP--YEWAGDSWVLFPSHPADYTPVCTTELGVARLPE 58
 QY 60 FTKKNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEK 119
 DB 59 FEKRNKVLALSVDSESHLGMKIDEEV--NNVKVDYPILADEKVKSTLYDMIHNSL 116
 QY 120 DKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWT 179
 DB 117 NN----LTVRTVTIIDPQKRLRTMTYPTASTGRNFAEILRVLDLSQLTQNYSVATPANWQ 172
 QY 180 AGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYRLTDPD 221
 DB 173 EGQECVIVPSLSDEAKQKPFKGFNAV-----KPYRLRTPOQ 209

RESULT 39

Q694A7
 ID Q694A7 PRELIMINARY; PRT; 220 AA.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:35:13 ; Search time 40 Seconds
(without alignments)
536.408 Million cell updates/sec

Title: US-10-723-123-3

Perfect score: 1194

Sequence: 1 MPLNLGDSFPDFOAEALGAE.....EALQLPSGKPYLRLTPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508.5	42.6	220	2 T03967	RAB24 protein - ri
2	497.5	41.7	212	2 G83215	probable antioxidant
3	495	41.5	218	2 S60285	B15C protein - bar
4	492	41.2	211	2 S77532	rehydrin - Syncho
5	478	40.0	202	2 S22499	hypothetical prote
6	458.5	38.4	212	2 AD2356	AhpC/TSA family pr
7	437	36.5	243	2 T18224	rehydrin protein h
8	420	35.2	261	2 S39825	hypothetical prote
9	403	33.8	218	2 AH2758	conserved hypothet
10	403	33.8	218	2 E97539	rehydrin (imported
11	400	33.5	219	2 A95978	probable anti-oxid
12	330.5	27.7	222	2 E70374	alkyl hydroperoxid
13	290.5	24.3	195	2 F69283	alkyl hydroperoxid
14	285.5	23.9	222	2 H64391	alkyl hydroperoxid
15	283.5	23.7	215	2 H72330	hypothetical prote
16	271	22.7	215	2 S74033	alkyl hydroperoxid
17	262	21.9	226	2 B69079	alkyl hydroperoxid
18	261.5	21.9	216	2 C71065	probable alkyl hyd
19	258.5	21.6	209	2 S51098	probable alkyl hyd
20	258.5	21.6	216	2 C75081	probable peroxid
21	248.5	20.8	250	2 B72454	probable thiorodox
22	240	20.1	242	2 S49173	hypothetical prote
23	235.5	19.7	210	2 T06318	thiol-specific ant
24	225.5	18.9	265	2 T09211	bas1 protein - spi
25	220	18.4	181	2 AD1638	2-cys peroxidexoi
26	219	18.3	197	2 C84951	alkyl hydroperoxid
27	218	18.3	197	2 AD1275	2-cys peroxidexoi
28	215	18.0	195	2 A43858	alkyl hydroperoxid
29	213	17.8	195	2 S71013	alkyl hydroperoxid

30	213	17.8	195	2 B70679	alkyl hydroperoxid
31	209	17.5	180	2 B69867	2-cys peroxidexoi
32	205.5	17.2	178	2 S29119	hypothetical prote
33	204.5	17.1	183	2 A83983	2-cys peroxidexoi
34	203	17.0	203	2 A12385	peroxidexoin (imp
35	202.5	17.0	226	2 S43598	mers homolog R07E5
36	202	16.9	200	2 S76284	hypothetical prote
37	199.5	16.7	195	2 E87164	alkyl hydroperoxid
38	197.5	16.5	195	2 G71492	probable thio-spec
39	195.5	16.4	198	2 C64715	alkyl hydroperoxid
40	195	16.3	200	2 I51016	proliferation asso
41	193.5	16.2	188	2 D71314	probable alkyl hyd
42	193	16.2	196	2 H86587	thio-specific anti
43	193	16.2	196	2 E72036	thio-specific anti
44	191.5	16.0	198	2 H71801	probable peroxid
45	191	16.0	199	2 A48513	macrophage 23K str

ALIGNMENTS

RESULT 1

T03967

RAB24 protein - rice

C;Species: Oryza sativa (rice)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T03967; PC4271

R;Fujino, K.; Tanaka, K.; Xu, Z.; Kikuta, Y.

submitted to the EMBL Data Library, August 1997

A;Description: ABA-responsive 24kDa polypeptide from rice calli is related to the thiol

A;Reference number: Z15166

A;Accession: T03967

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-220 <FUJ>

A;Cross-references: UNIPROT:P52573; EMBL:D63917; PIDN:BAA09947.1

A;Experimental source: cv. Yuhkara

R;Kawakami, T.; Kamo, M.; Chen, M.C.; Taugita, A.

submitted to JIPID, April 1997

A;Reference number: PC4267

A;Accession: PC4271

A;Molecule type: protein

A;Residues: 2-15 <KAW>

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro

Query Match 42.6%; Score 508.5; DB 2; Length 220;

Best Local Similarity 43.6%; Pred. No. 1.6e-38;

Matches 96; Conservative 46; Mismatches 73; Indels 5; Gaps 4;

Qy 1 MP-LNLGDSFPDFOAEALGAEHRLHEYLGDSDGVMFSDHNDFTPVCTTLEAEAVKLQDS 59

Db 1 MPGLTGDTVPNLELSTHGK-IRIHDVGDVTVILFSPHGDFTPVCTTLEAAMAAYAKE 59

Qy 60 FTKNCKLVGFCNDLQSHREAWKIDIMAYAGRSNGN-LPPFLVCDPNRELAASIGIMDPAE 118

Db 60 FDRKGVKLLGISCDVQSHKDFKDEAY--KPGNRVTVYIMADPSREAIKQLNMVDPDE 117

Qy 119 KDKKGLPLTCRCVFFISPEKLAASILYPATTCGNFAEILRVLDLSLQLTAKFPVATPDV 178

Db 118 KDSNGGHLPSRALHIVGPDKKVLSFLYPACVGRNMDVVRAVDALQTAARLATPVNW 177

Qy 179 TAGAKCVVPLAAEAQRLLPKGHEALQLPSGKPYLRLT 218

Db 178 KPGEFPVIPGVSDDEAKEKFPQGFDTADLPSSGKGYLRFT 217

RESULT 2

G83215

probable antioxidant protein PA3450 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: G83215

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; E

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 <STO>
A;Cross-references: UNIPROT:Q9HYF6; GB:AE004765; GB:AE004091; NID:g9949580; PIDN:AAG0683
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3450
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 41.7%; Score 497.5; DB 2; Length 212;
Best Local Similarity 46.8%; Pred. No. 1.5e-37;
Matches 104; Conservative 34; Mismatches 71; Indels 13; Gaps 5;

QY 1 MPNLGDSFPDFAEALGAHFLRHLHEYLGDGSGVMFSPHNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLGDIAPDFEQDS-SEGRIRLHEWLGDGSGVFLFSPADFTPVCTTTELGFATAKLQDF 59

QY 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKD 120
Db 60 AQGVKVLALUSDVPVESHKWKIIDDINETQTRVN--FPITADADRKVSELDYDIHNAND 117

QY 121 KKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDTWA 180
Db 118 ---TLTVRSFLIIDPSKKVRLIITYPASTGRNFNEILRVLDLSQLTDEHKVATPANWED 173

QY 181 GAKCCVVPNLA-ABEAQRLLPKGHEALQLPSGKPYLRLTPDP 221
Db 174 GDEWIVPSLKDEEIKRRFPKGYRAV-----KPYLRLTPQP 210

RESULT 3
S60285
B5C protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S60285
R;Aalen, R.B.; Opsahl-Ferstad, H.G.; Linnestad, C.; Olsen, O.A.
Plant J. 5, 385-396, 1994
A;Title: Transcripts encoding an oleosin and a dormancy-related protein are present in barley
A;Reference number: S60284; MUID:94236153; PMID:8180622
A;Accession: S60285
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-218 <AAL>
A;Cross-references: UNIPROT:PS2572; EMBL:X76605; NID:g471320; PIDN:CAA54066.1; PID:g4713
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

Query Match 41.5%; Score 495; DB 2; Length 218;
Best Local Similarity 43.4%; Pred. No. 2.7e-37;
Matches 95; Conservative 43; Mismatches 77; Indels 4; Gaps 4;

QY 1 MP-LNLGDSFPDFAEALGAHFLRHLHEYLGDGSGVMFSPHNDFTPVCTTTELAEAVKLQDS 59
Db 1 MPGLTIGDTPVNLDELSTHGK-IRIHDYGVNGVILFSPHGDFTPVCTTTELAAMANYAKE 59

QY 60 FTKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEK 119
Db 60 FEKRGVLLGISCDVDVQSHKEWTNDIEAYKPGS-KVTYPTIMADPDRSAIKQLNMVDPDEK 118

QY 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVATPVDTW 179
Db 119 DAQG-QLPSTLHIVGPKVKLSFLYPSCTGRNMDEVRVDSLLTAAKHVATPANWK 177

QY 180 AGAKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYLRLT 218
Db 178 PGECWVIAPGVDSBEAKMFPQGFETADLPSSKGYLRAFT 216

RESULT 4

S77532

rehydriin - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein slr1198

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S77532

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77532

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-211 <KAN>

A;Cross-references: UNIPROT:P73348; EMBL:D90905; GB:AB001339; NID:gl652360; PIDN:BAAL173

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH2758
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
star, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH2758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KUR>
A;Cross-references: UNIPROT:Q8UF88; GB:AB008688; PIDN:AAL42486.1; PID:g17739903; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul480
A;Map position: circular chromosome
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.8%; Score 403; DB 2; Length 218;
Best Local Similarity 39.4%; Pred. No. 5.5e-29;
Matches 89; Conservative 31; Mismatches 92; Indels 14; Gaps 4;
QY 1 MPLNLGDSPPDFOAALGAHFLRHLHYLGDSWGMFSDHNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLINDIADPDFTAETTQGP-VRFPHDWIGDGMVLFSPHKNFTFPVCTTELGA MGGLQPEF 59
QY 61 TKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELA-----ASLGIMD 115
Db 60 EKRGVKIIGISVDPVESHKWKADIRTAGT--FNVDYPLIGDKDLKVKALYDMLPAGAGD 117
QY 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
Db 118 SSGERTPADNATVRSVFGPKKIKLVLTYPMTTGRNFDLRAIDSLQTSKHQVATP 177
QY 176 VDMTAGKCCVVPNLAAEBAQRLLPKGHEALQLPSPGKPYRLRTPDP 221
Db 178 ANWKGEDVIITAASVNEAIAIRFGSYDTVL-----PYLRKTKQP 217
RESULT 10
E97539
rehydrin [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97539
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E97539
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KUR>
A;Cross-references: UNIPROT:Q8UF88; GB:AB007869; PIDN:AAK87270.1; PID:g15156560; GSPDB:G
C;Genetics:
A;Gene: AGR C 2729
A;Map position: circular chromosome
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.8%; Score 403; DB 2; Length 218;
Best Local Similarity 39.4%; Pred. No. 5.5e-29;
Matches 89; Conservative 31; Mismatches 92; Indels 14; Gaps 4;
QY 1 MPLNLGDSPPDFOAALGAHFLRHLHYLGDSWGMFSDHNDFTPVCTTTELAEAVKLQDSF 60
Db 1 MSRLINDIADPDFTAETTQGP-VRFPHDWIGDGMVLFSPHKNFTFPVCTTELGA MGGLQPEF 59
QY 61 TKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELA-----ASLGIMD 115

Db 60 EKRGVKIIGISVDPVESHKWKADIRTAGT--FNVDYPLIGDKDLKVKALYDMLPAGAGD 117
QY 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
Db 118 SSGERTPADNATVRSVFGPKKIKLVLTYPMTTGRNFDLRAIDSLQTSKHQVATP 177
QY 176 VDMTAGKCCVVPNLAAEBAQRLLPKGHEALQLPSPGKPYRLRTPDP 221
Db 178 ANWKGEDVIITAASVNEAIAIRFGSYDTVL-----PYLRKTKQP 217
RESULT 11
A95978
probable anti-oxidant protein, AhpCTS family [imported] - Sinorhizobium meliloti (stra
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95978
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: A95978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <KUR>
A;Cross-references: UNIPROT:Q9R9R2; GB:AL591985; PIDN:CAC49489.1; PID:g15140976; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yen, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20964
A;Genome: plasmid
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 33.5%; Score 400; DB 2; Length 219;
Best Local Similarity 40.6%; Pred. No. 1e-28;
Matches 93; Conservative 33; Mismatches 83; Indels 20; Gaps 8;
QY 1 MPLNLGDSPPDFOAALGAHFLRHLHYLGDSWGMFSDHNDFTPVCTTTELAEAVKLQDS 59
Db 1 MSRLINDIADPDFTAETTQGTINF--HEWIGDGMVLFSPHKNFTPVCTTELGA MGAGIEPE 58
QY 60 FTKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFLVCDPNREL--AASLGIMDPA-- 117
Db 59 FRKRGVKIIGISVDPVESHKWKNDIKVATG--FEVDYPLIGD--RDLKVKALYDMLPAG 114
QY 118 --EKDKKGLP---LTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPV 172
Db 115 AGTSEGRTPADNATVRSVYVIGPKKIKLVLTYPMTTGRNFEILRAIDSLQLTAKH 174
QY 173 ATPVDWTAGAKCCVVPNLAAEBAQRLLPKGHEALQLPSPGKPYRLRTPDP 221
Db 175 ATPANWQGEDVIITAASVNEAIAIRFGSFDTVL-----PYLRKTKQP 217
RESULT 12
E70374
alkyl hydroperoxide reductase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: E70374
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Gra
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320

QY 61 TKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKD 120
Db 63 RKLNTELGISIDQVFSHIKWIEMKELG--VEIEFPVIADDLGVSRRLLGIHP----- 116
QY 121 KKGPLTCTCRVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDTA 180
Db 117 NKGTN--TVRAVFVDNGIIRALVYYPQEVGRNIDILRAVRALQTSDBKGVAIPANWPS 175
QY 181 GA----KCCVVPNLAEEAQRLL 199
Db 176 NELINDSVIIPPASSVEEARKRL 198
RESULT 16
S74033
alkyl hydroperoxide reductase homolog - Sulfolobus solfataricus
N;Alternate names: protein c0215
C;Species: Sulfolobus solfataricus
C;Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S74033
R;Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.
Mol. Microbiol. 22, 175-191, 1996
A;Title: Organizational characteristics and information content of an archaeal genome: 1
A;Reference number: S73076; MUID:97055432; PMID:8899719
A;Accession: S74033
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <GEN>
A;Cross-references: UNIPROT:P95895; EMBL:Y08256; NID:g1707679; PID:CAA69447.1; PID:g170
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 pro
Query Match 22.7%; Score 271; DB 2; Length 215;
Best Local Similarity 31.4%; Pred. No. 4.6e-17;
Matches 69; Conservative 35; Mismatches 88; Indels 28; Gaps 7;
QY 1 MPLNLGDSFPDFOAEALGAEHFRLHYLGDSWGMFSPNDFTPVCTTTELAEAVKLQDSF 60
Db 6 IPL-IGERFPPEMEVITTOGRKLPDDYKG-RWPFVLSHPGDFTPVCTTFYSFAKKYEEF 63
QY 61 TKNCKLVGSCNDLQSHREW----AKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMD 116
Db 64 KKLNTELGISVDSNISHIEMWIEKNLV-----EIPFPPIADPMGNVAKRLGMI-- 115
QY 117 AEKDKKGLPLTCTCRVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 176
Db 116 ---HAQSSTATVRAVFVDDKGVRLLIYYPMIEGRNIDILRAIRALQLVDRAGVVTPA 172
QY 177 DWTAGAKCCVVPN--LAEEAQRLLPKGHEALQLPSGKPY 214
Db 173 NW-----PNNELIGDKVINPAPRTIKDKAKWRLGQPF 203
RESULT 17
B69079
alkyl hydroperoxide reductase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C;Accession: B69079
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A6900; MUID:98037514; PMID:9371463
A;Accession: B69079
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-226 <MTH>
A;Cross-references: GB:AE000804; GB:AE000666; NID:g2621196; PID:AA84665.1; PID:g262120
A;Experimental source: strain Delta H

C;Genetics:
A;Gene: MTH159
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
Query Match 21.9%; Score 262; DB 2; Length 226;
Best Local Similarity 33.7%; Pred. No. 3.2e-16;
Matches 60; Conservative 33; Mismatches 75; Indels 10; Gaps 5;
QY 1 MPLNLGDSFPDFOAEALGAEHFRLHYLGDSWGMFSPNDFTPVCTTTELAEAVKLQDSF 60
Db 18 MPL-IGDKFPPEMEVQTGPMELPDDEFEG-KWFIILFSPADFTPVCTTFEYVAFQEVYPEL 75
QY 61 TKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPAEKD 120
Db 76 RELDCELGLSLVDQVFSHIKWIETIA--ENLDETEFFPVIA DTGR-VADTLGLIHPART 132
QY 121 KKGPLTCTCRVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 178
Db 133 N-----TVRAVFVDPEGIIRALVYYPQELGRNIEIVRMIRAFRVIDAEGVAAPANW 185
RESULT 18
C71065
probable alkyl hydroperoxide reductase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: C71065
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki;
M.; Ohfuku, Y.-Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71065
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-216 <KAW>
A;Cross-references: UNIPROT:O58966; GB:AP000005; NID:g3236132; PID:BAA30317.1; PID:g32
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1217
Query Match 21.9%; Score 261.5; DB 2; Length 216;
Best Local Similarity 32.4%; Pred. No. 3.3e-16;
Matches 66; Conservative 36; Mismatches 77; Indels 25; Gaps 7;
QY 5 LGDSFPDFOAEALGAEH--FRLHEYL--GDSWGMFSPNDFTPVCTTTELAEAVKLQDSF 60
Db 4 IGEKFPPEVEVK---TTHGVIKLPDYFTKQGWFIILFSPADFTPVCTTFEYGMQKRVVEF 60
QY 61 TKNCKLVGSCNDLQSH---REWAKDIMAYAGRSNLPFPPLVCDPNRELAASLGIMDPA 117
Db 61 RKLGVPEIGLSVDQVFSHIKWIENKDLN----SVEIDFPVIADDRGELAEKLGMI--- 112
QY 118 EKDKKGLPLTCTCRVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPV 177
Db 113 ----PSGATITARAVFVDDKGIRALVYYPAEVGRDWDIELRVKALKISTEKGVALPHK 169
QY 178 W-----TAGAKCCVVPNLAEEAQR 197
Db 170 WPNNELIGDKVINPVPASTIEKKQ 193
RESULT 19
S51098
probable alkyl hydroperoxide reductase (EC 1.6.4.-) - Methanobacterium thermoautotroph
N;Alternate names: hypothetical protein k
C;Species: Methanobacterium thermoautotrophicum
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S51098
R;Meile, L.; Fischer, T.
submitted to the EMBL Data Library, July 1993
A;Description: Molecular characterization of a superoxide dismutase gene from Methanoba

A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: ahpC; BU182
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 18.3%; Score 219; DB 2; Length 197;
Best Local Similarity 30.5%; Pred. No. 2.1e-12;
Matches 54; Conservative 29; Mismatches 82; Indels 12; Gaps 3;

Qy 10 PDFQAEAL-----CAEHFRLHEYLGDGSGVMFSPNDFTPVCTTELAEAVKLQDSFTKKN 64
Db 9 PNFTAPAILKNNQIVEQFDLKKYSNGOSTVLFFWPMDFTFVCPSEIIEFNKLHSEFKRN 68
Qy 65 CKLVGFSNDLQSHREWAKDIMAYAGRSGLNPPPLVCDPNRELAASIGINDPAEKOKKGL 124
Db 69 KVIVGVSDSVVYHQAW-QNTLPKNGGIGKINFPWSDVVKHDIQKSGIOHP-----NL 121
Qy 125 PLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATVPDWTAG 181
Db 122 GIALRASFLDSNWIIRHQVVNDLPFCGRNITDMRWYDALDFHNKGEVCPANWKG 178

RESULT 27
AD1275
2-cys peroxiredoxin homolog lmol604 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1275
R:Glaser, P.; Fraigneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1275
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <GLA>
A:Cross-references: UNIPROT:Q8Y6S9; GB:NC_003210; PIDN:CAC99682.1; PID:g16411033; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmol604
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 18.3%; Score 218; DB 2; Length 181;
Best Local Similarity 28.9%; Pred. No. 2.3e-12;
Matches 54; Conservative 37; Mismatches 80; Indels 16; Gaps 6;

Qy 5 LGDSFPDFQAEALGAEH-----FRLHEYL-GDSGVMFSPNDFTPVCTTELAEAVKLQDS 59
Db 6 VGTQAPRFEMAEVAMPNPTFGKVSLEKNIEDDKWTILFFYPMDFTFVCPTEIVSAISARSD 65
Qy 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSGLNPPPLVCDPNRELAASIGINDPAEK 119
Db 66 FDLNARIIIGASTDITTHSLAWNTPTIKEGG-IGKLNYPAAADTNHQVASDYGL-----I 120
Qy 120 DKKGLPUTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATVPDWT 179
Db 121 EEEGVAL--RGLFTINPKGIQIEVHHNIGREVDLRLVQLQTGG-----LCPINQ 174
Qy 180 AGAKCCV 186
Db 175 PGEKTIV 181

RESULT 28
A43858
alkyl hydroperoxidase C (EC 1.6.4.-) - Mycobacterium avium

N:Alternate names: Avi-3 antigen
C:Species: Mycobacterium avium
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43858; T09655
R:Yamaguchi, R.; Matuo, K.; Yamazaki, A.; Takahashi, M.; Fukasawa, Y.; Wada, M.; Abe, I.
Infect. Immun. 60, 1210-1216, 1992
A:Title: Cloning and expression of the gene for the Avi-3 antigen of Mycobacterium avium
A:Reference number: A43858; MUID:92175967; PMID:1371765
A:Accession: A43858
A:Status: preliminary
A:Title: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <YAM>
A:Cross-references: UNIPROT:Q57413; GB:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g8411
A:Note: sequence extracted from NCBI backbone (NCBIN:85445, NCBIP:85446)
R:Sherman, D.R.; Sabo, P.J.; Hickey, M.J.; Arain, T.M.; Mahairas, G.G.; Yuan, Y.; Barry
Proc. Natl. Acad. Sci. U.S.A. 92, 6625-6629, 1995
A:Title: Disparate responses to oxidative stress in saprophytic and pathogenic mycobact
A:Reference number: Z16801; MUID:95327698; PMID:7604044
A:Accession: T09655
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <SHE>
A:Cross-references: EMBL:U18263; NID:g1040852; PIDN:AAA79917.1; PID:g841168
C:Genetics:
A:Gene: ahpC
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
C:Keywords: oxidoreductase
F:23-162/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 18.0%; Score 215; DB 2; Length 195;
Best Local Similarity 31.0%; Pred. No. 4.7e-12;
Matches 57; Conservative 32; Mismatches 61; Indels 34; Gaps 7;

QY 1 MP-LNLGDSPPDQAEALGA-----BHPRL---HEVLGDSWGMFSPNDFTF 44
DB 1 MPLLTTIGDQPPAYELTALTATAGDLSKVDAKQPGDYFTTITSEDHAG-KWRVVFVFPKDFTE 59

QY 45 VCTTEALAEAVKLDQSFTEKKNCKLVGFSCNDLQSHREWA---KDTMAYAGRSNLPFPPLVC 101
DB 60 VCTETATATGKLNDEFDRDAQVLGVSIDSEFVHFNWRAQHEDLK-----NLFPFMLS 112

QY 102 DPNRELAASIGIMDPAEKOKKGLPLTRCVRFFISPEKKLAASILYPATTGRNFAEILRLV 161
DB 113 DIKRELSLATGVNLAD-----GVADRATFIVDPNNEIQFVSVTAGSVGRNVEEVLRLV 165

QY 162 DSLQ 165
DB 166 DALQ 169

RESULT 29
S71013
alkyl hydroperoxide reductase chain C - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C:Accession: S71013; S71011
R:Wilson, T.M.; Collins, D.M.
Mol. Microbiol. 19, 1025-1034, 1996
A:Title: ahpC, A gene involved in isoniazid resistance of the Mycobacterium tuberculosis
A:Reference number: S71011; MUID:96249696; PMID:8830260
A:Accession: S71013
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-195 <WIL>
A:Cross-references: UNIPROT:Q57348; EMBL:U24083; NID:g1002370; PIDN:AAB60203.1; PID:g10
A:Experimental source: ATCC 35723
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A:Accession: S71011
A:Molecule type: DNA
A:Residues: 1-195 <WIL>
A:Cross-references: EMBL:U24084; NID:g1002373; PIDN:AAB38112.1; PID:g1002374
A:Experimental source: ATCC 35729
A:Genetics:

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 21:53:05 ; Search time 167 Seconds
(without alignments)
558.225 Million cell updates/sec

Title: US-10-723-123-3
Perfect score: 1194
Sequence: 1 MPLNLGDSFPDFAEALGAE.....EALQLPSGKPYRLRLTPDRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*

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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*

19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1194	100.0	223	17 US-10-723-123-3	Sequence 3, Appli
2	707	59.2	224	17 US-10-732-923-21412	Sequence 21412, A
3	669.5	56.1	224	17 US-10-732-923-21334	Sequence 21334, A
4	653.5	54.7	224	9 US-09-728-914-37	Sequence 37, Appl
5	653.5	54.7	224	17 US-10-732-923-21440	Sequence 21440, A
6	645.5	54.1	224	17 US-10-732-923-21438	Sequence 21438, A
7	644	53.9	220	17 US-10-732-923-21431	Sequence 21431, A
8	640.5	53.6	224	9 US-09-819-505-4	Sequence 4, Appli
9	640.5	53.6	224	17 US-10-732-923-21327	Sequence 21327, A
10	640.5	53.6	224	17 US-10-732-923-21328	Sequence 21328, A
11	640.5	53.6	235	17 US-10-732-923-21415	Sequence 21415, A

12	638.5	53.5	224	9 US-09-728-914-38	Sequence 38, Appl
13	638.5	53.5	224	9 US-09-819-505-2	Sequence 2, Appli
14	638.5	53.5	224	9 US-09-981-353-4	Sequence 4, Appli
15	638.5	53.5	224	14 US-10-205-823-198	Sequence 198, App
16	638.5	53.5	224	16 US-10-851-921-16	Sequence 16, Appl
17	638.5	53.5	224	17 US-10-502-279-8	Sequence 8, Appli
18	638.5	53.5	224	17 US-10-651-056-3	Sequence 3, Appli
19	638.5	53.5	224	17 US-10-732-923-21433	Sequence 21433, A
20	638.5	53.5	224	20 US-11-051-454-198	Sequence 198, App
21	636	53.3	220	17 US-10-732-923-21325	Sequence 21325, A
22	634.5	53.1	224	17 US-10-732-923-21329	Sequence 21329, A
23	630.5	52.8	224	17 US-10-732-923-21434	Sequence 21434, A
24	626.5	52.5	224	17 US-10-732-923-21330	Sequence 21330, A
25	625.5	52.4	217	17 US-10-732-923-21202	Sequence 21202, A
26	619.5	51.9	219	17 US-10-732-923-21255	Sequence 21255, A
27	619	51.8	221	9 US-09-728-914-2	Sequence 2, Appli
28	619	51.8	221	17 US-10-732-923-21259	Sequence 21259, A
29	618.5	51.8	235	17 US-10-732-923-21419	Sequence 21419, A
30	617.5	51.7	235	9 US-09-728-914-39	Sequence 39, Appl
31	617.5	51.7	235	17 US-10-732-923-21418	Sequence 21418, A
32	609.5	51.0	222	17 US-10-732-923-21155	Sequence 21155, A
33	607.5	50.9	224	17 US-10-732-923-21331	Sequence 21331, A
34	599	50.2	232	17 US-10-732-923-21416	Sequence 21416, A
35	595.5	49.9	249	17 US-10-732-923-21349	Sequence 21349, A
36	588	49.2	222	17 US-10-732-923-21422	Sequence 21422, A
37	588	49.2	222	17 US-10-732-923-21423	Sequence 21423, A
38	587	49.2	222	20 US-11-097-143-5670	Sequence 5670, Ap
39	587	49.2	222	17 US-10-732-923-21424	Sequence 21424, A
40	575	48.2	216	17 US-10-732-923-21413	Sequence 21413, A
41	572.5	47.9	219	17 US-10-732-923-21118	Sequence 21118, A
42	535.5	44.8	219	17 US-10-732-923-21387	Sequence 21387, A
43	533	44.6	250	15 US-10-424-599-206910	Sequence 206910,
44	529	44.3	222	16 US-10-767-701-45566	Sequence 45566, A
45	521.5	43.7	248	17 US-10-732-923-21350	Sequence 21350, A

ALIGNMENTS

RESULT 1

US-10-723-123-3

; Sequence 3, Application US/10723123

; Publication No. US20050037020A1

; GENERAL INFORMATION:

; APPLICANT: Akzo Nobel N.V.

; TITLE OF INVENTION: Coccidiosis vaccines

; NUMBER OF SEQUENCES: 41

; STREET: Velperweg 76

; CITY: Arnhem

; COUNTRY: The Netherlands

; ZIP: 6824 BM

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/723,123

; FILING DATE: 26-Nov-2003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 0412 666379

; TELEFAX: 0412 650592

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 223 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-723-123-3

Query Match 100.0%; Score 1194; DB 17; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.7e-126; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0;

QY 1 MPLNLGDSFPDFOAEALGAHFRHLHEYLGDGSGWGMFMSHPNDFTPVCTTTELAEAVKLQDSF 60
DB 1 MPLNLGDSFPDFOAEALGAHFRHLHEYLGDGSGWGMFMSHPNDFTPVCTTTELAEAVKLQDSF 60

QY 61 TKKNCKLVGFSNCDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
DB 61 TKKNCKLVGFSNCDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPVVDWTA 180
DB 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPVVDWTA 180

QY 181 GAKCCVVPNLAAEAAQRLPKGHEALQLPKGKPYLRLTPDP 223
DB 181 GAKCCVVPNLAAEAAQRLPKGHEALQLPKGKPYLRLTPDP 223

RESULT 2

US-10-732-923-21412
; Sequence 21412, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21412
; LENGTH: 224
; TYPE: PRP
; ORGANISM: Toxoplasma gondii
US-10-732-923-21412

Query Match 59.2%; Score 707; DB 17; Length 224;
Best Local Similarity 57.0%; Pred. No. 2.9e-71;
Matches 126; Conservative 36; Mismatches 57; Indels 2; Gaps 1;

QY 3 LNLGDSFPDFOAEALG--ABHFRHLHEYLGDGSGWGMFMSHPNDFTPVCTTTELAEAVKLQDSF 60
DB 2 LVLGSTPPDVHADSGVPGDKIKLYDPLGDSWGLMSHPDFTPVCTTTELAAQARMAPEF 61

QY 61 TKKNCKLVGFSNCDLQSHREWAKDIMAYAGRSNGLPPLVCDPNRELAASLGIMDPAEKD 120
DB 62 AKRCKLIGFSCDDVSHKGWAKDVMVSKLSDGLPPIADPERKLTATDLGIMDPEEKD 121

QY 121 KKGGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATPVVDWTA 180
DB 122 KAGIPVTCRAAIYIGPDRRVKGLILYPATVGRNFKEVLRALDALQAEKYPVATPGWFP 181

QY 181 GAKCCVVPNLAAEAAQRLPKGHEALQLPKGKPYLRLTPDP 221
DB 182 GDKVMVQPTLTDBEAKAKPKGFEKKCEKPSGKNLYRYADP 222

RESULT 3

US-10-732-923-21334
; Sequence 21334, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21334
; LENGTH: 224
; TYPE: PRP
; ORGANISM: Rattus norvegicus
US-10-732-923-21334

Query Match 56.1%; Score 669.5; DB 17; Length 224;
Best Local Similarity 58.0%; Pred. No. 5.2e-67;
Matches 131; Conservative 29; Mismatches 59; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDFOAE--ALGAHFRHLHEYLGDGSGWGMFMSHPNDFTPVCTTTELAEAVKLQ 57
DB 1 MPGGLLLGDEAPNFEANTTIG--HTRFHDYLGDSWGLFMSHPDFTPVCTTTELGRAAKLA 58

QY 58 DSFTKKNCKLVGFSNCDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
DB 59 PEFAKENVKIALSIDSVEDHFAWSKDINAYNGAAPTEKLPFIIDDKORDLAAILGMLD 118

QY 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
DB 113 PAEKDEKGMPTARVVFIQPKKLSILYPATTGRNFDILRVVDSLQLTASNVPVATP 178

QY 176 VDWTAGAKCCVVPNLAAEAAQRLPKGHEALQLPKGKPYLRLTPDP 221
DB 179 VDMKGESVMVLTLPPEEAKQLFPKGVFTKELPSGKYLRYTPQ 224

RESULT 4

US-09-728-914-37
; Sequence 37, Application US/09728914
; Patent No. US2001004699A1
; GENERAL INFORMATION:
; APPLICANT: KANTOR, FRED S.
; APPLICANT: FIKRIG, EROL
; APPLICANT: DAS, SUBRATA
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
; TITLE OF INVENTION: THEM
; FILE REFERENCE: YU-107
; CURRENT APPLICATION NUMBER: US/09/728,914
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/169,048
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/240,716
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 224
; TYPE: PRP
; ORGANISM: Bovine sp.
US-09-728-914-37

Query Match 54.7%; Score 653.5; DB 9; Length 224;
Best Local Similarity 56.6%; Pred. No. 3.4e-65;
Matches 128; Conservative 30; Mismatches 61; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDFOAE--ALGAHFRHLHEYLGDGSGWGMFMSHPNDFTPVCTTTELAEAVKLQ 57
DB 1 MPGGLLLGDEAPNFEANTTIG--RIRFHDYLGDSWGLFMSHPDFTPVCTTTELGRAAKLA 58

QY 58 DSFTKKNCKLVGFSNCDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
DB 59 PEFAKENVKIALSIDSVEDHFAWSKDINAYNGEEPTEKLPFIIDDKORDLAAILGMLD 118

QY 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVDSLQLTAKFPVATP 175
DB 119 PAEKDEKGMPTARVVFIQPKKLSILYPATTGRNFDILRVVDSLQLTAKRVATP 178

QY 176 VDWTAGAKCCVVPNLAAEAAQRLPKGHEALQLPKGKPYLRLTPDP 221
DB 179 VDMKNGDSVMVLTPIPEEAKKLPKGVFTKELPSGKYLRYTPQ 224

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RESULT 5
US-10-732-923-21440
; Sequence 21440, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21440
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-732-923-21440
Query Match 54.7%; Score 653.5; DB 17; Length 224;
Best Local Similarity 56.6%; Pred. No. 3.4e-65;
Matches 128; Conservative 30; Mismatches 61; Indels 7; Gaps 4;

Qy 1 MP--LNLGSDPPDQAB-ALGAEHRLHEYLGDGSGVMFSDHNDFTPVCTTELAEAVKLQ 57
Db 1 MPGLLLGDEAPNFANFTTIG--RIRFHDYLDGSGWILFSDHNDFTPVCTTELGRAAKLA 58

Qy 58 DSFTKKNCKLVGFSNDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
Db 59 PEFARNVKMIALSIDSVEDHLAWSKDINAYNGEETKLPFFPIIDDKRDLAIFQLGMLD 118

Qy 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
Db 119 PAEKDEKGMPTARVVFIFGDKKLLSILYPATTGRNFAEILRVLSQLTAEKRVATP 178

Qy 176 VDMTAGKCCVVPNLAAEEAQRLLPKGHEALQLPSPGKPYRLTDPD 221
Db 179 VDMKNGDSVMVLPITPEEAKLPFGVFTKELPSGKKYLYRTPQP 224

RESULT 6
US-10-732-923-21438
; Sequence 21438, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21438
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-732-923-21438
Query Match 54.1%; Score 645.5; DB 17; Length 224;
Best Local Similarity 55.8%; Pred. No. 2.8e-64;
Matches 126; Conservative 32; Mismatches 61; Indels 7; Gaps 4;

Qy 1 MP--LNLGSDPPDQAB-ALGAEHRLHEYLGDGSGVMFSDHNDFTPVCTTELAEAVKLQ 57
Db 1 MPGLLLGDEAPNFANFTTIG--RIRFHDYLDGSGWILFSDHNDFTPVCTTELGRAAKLA 58

Qy 58 DSFTKKNCKLVGFSNDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
Db 59 PEFARNVKMIALSIDSVEDHLAWSKDINAYNGEETKLPFFPIIDDKRDLAIFQLGMLD 118

Qy 116 PAEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
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Db 119 PAEKDEQGMPTARVVFIFGDKKLLSILYPATTGRNFAEILRVLSQLTAEKRVATP 178
Qy 176 VDMTAGKCCVVPNLAAEEAQRLLPKGHEALQLPSPGKPYRLTDPD 221
Db 179 VDMKNGDSVMVLPITPEEAKLPFGVFTKELPSGKKYLYRTPQP 224

RESULT 7
US-10-732-923-21431
; Sequence 21431, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21431
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Plasmodium yoelii yoelii
US-10-732-923-21431
Query Match 53.9%; Score 644; DB 17; Length 220;
Best Local Similarity 56.7%; Pred. No. 4e-64;
Matches 123; Conservative 31; Mismatches 61; Indels 2; Gaps 2;

Qy 1 MPLNLGSDPPDQAB-ALGAEHRLHEYLGDGSGVMFSDHNDFTPVCTTELAEAVKLQDS 59
Db 1 MGYHLGATFNFATAKSGIDGDFELYKIENSNAILFSDHNDFTPVCTTELAEGLCKHED 60

Qy 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEK 119
Db 61 FLKLNCKLIGFSCNSKESHDKIWEDI--KYGKLNKWEIPIVCDSERELANKLKIMDQEK 119

Qy 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPDWT 179
Db 120 DITGLPLTCRCVFFISPEKKIKATVLYPATTTGNAHEILRVLSQLTATTPVATPVNWN 179

Qy 180 AGAKCCVVPNLAAEEAQRLLPKGHEALQLPSPGKPYLR 216
Db 180 EGDKCCVIFTLQDDEISKHFKEITKVEPMSKKYLR 216

RESULT 8
US-09-819-505-4
; Sequence 4, Application US/09819505
; Patent No. US20020142417A1
; GENERAL INFORMATION:
; APPLICANT: Paigen, Beverly
; Beier, David R.
; TITLE OF INVENTION: Antioxidant Protein 2, Gene and Methods
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: P. O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/819,505
; FILING DATE: 28-Mar-2001
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Db 67 NVKLGSLCDSVQSHRWKADIIELCRMKSGDSNCCSGNKLPPPIIADNRSLSKLG 126
Qy 114 MDPAEKKGGLPLTCRCVFFISPEKLAASILYPAATGRNFAELRLVLDLSQLTAKPPVA 173
Db 127 MDPECEKGAALTARCLFIIGPKTKLSILYPAATGRNFDLRLVVDLSQLTATKLV 186
Qy 174 TPVDWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 222
Db 187 TPVDWQNGDDCVVPTINDNEAKLFGKINTVELPSGKPYLRVVAHPK 235

RESULT 12
US-09-728-914-38
; Sequence 38, Application US/09728914
; Patent No. US20010046499A1
; GENERAL INFORMATION:
; APPLICANT: KANTOR, FRED S.
; APPLICANT: FIKRIG, EROL
; APPLICANT: DAS, SUBRATA
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING
; FILE REFERENCE: YU-107
; CURRENT APPLICATION NUMBER: US/09/728,914
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/169,048
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/240,716
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-914-38

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
Qy 1 MP--LNLGDFPDFOAALGAHFRHLHEYLGDWSGVMSFHPNDFTPVCTTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNFEANTT-VGRIRFHDFLGDSNGILFSPHPRDFTPVCTTTELGRAAKLAP 59
Qy 59 SFTKKNCKLVGFCNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFARNVKKLALSIDSVEDHLAWSKOINAYNCEPTEKLPFPFIIDDRNRELAAILGLMDP 119
Qy 117 AEKDKKGLPLTCRCVFFISPEKLAASILYPAATGRNFAELRLVLDLSQLTAKPPVATPV 176
Db 120 AEKDEKMPVTARVVFVFGPKLKLILYPAATGRNFDLRLVVDLSQLTAEKRVATPV 179
Qy 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 221
Db 180 DWKDGDSVMVLPPIPEEAKLPKGVFTKELPSGKKYLRYTQ 224

RESULT 13
US-09-819-505-2
; Sequence 2, Application US/09819505
; Patent No. US20020142417A1
; GENERAL INFORMATION:
; APPLICANT: Paigen, Beverly
; TITLE OF INVENTION: Antioxidant Protein 2, Gene and Methods
; of Use Therefor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Farrell & Associates
; STREET: P. O. Box 999
; CITY: York Harbor
; STATE: ME

COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/819,505
FILING DATE: 28-Mar-2001
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: JL-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-819-505-2

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;
Qy 1 MP--LNLGDFPDFOAALGAHFRHLHEYLGDWSGVMSFHPNDFTPVCTTTELAEAVKLQD 58
Db 1 MPGLLLGDVAPNFEANTT-VGRIRFHDFLGDSNGILFSPHPRDFTPVCTTTELGRAAKLAP 59
Qy 59 SFTKKNCKLVGFCNDLQSHREWAKDIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFARNVKKLALSIDSVEDHLAWSKOINAYNCEPTEKLPFPFIIDDRNRELAAILGLMDP 119
Qy 117 AEKDKKGLPLTCRCVFFISPEKLAASILYPAATGRNFAELRLVLDLSQLTAKPPVATPV 176
Db 120 AEKDEKMPVTARVVFVFGPKLKLILYPAATGRNFDLRLVVDLSQLTAEKRVATPV 179
Qy 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTDP 221
Db 180 DWKDGDSVMVLPPIPEEAKLPKGVFTKELPSGKKYLRYTQ 224

RESULT 14
US-09-981-353-4
; Sequence 4, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Laese, Amy W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 3200830CD1
US-09-981-353-4

Query Match 53.5%; Score 638.5; DB 9; Length 224;
Best Local Similarity 56.4%; Pred. No. 1.7e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

Qy	1	MP--LNLGDSFPDQEAALGAEBHFLRHHYVLGDSWGVMFSPHNDFTPVCTTTELAEAVKLO	58
Db	1	MPGGLLGLGVAPNFEANTT-VGRIRFHDFLGDSWGILFHSHPDFTPVCTTTELGRAAKLAP	59
Qy	59	SFTKKNKLVGSCNDLQSHREWAKDINAY--AGRSQNLPEPLVCDNRLEASLGIMDP	116
Db	60	EFAKRNKVLTAUSIDVEDHLAWSKDINAYNCBETKLPPIIDDRNRELATLLGMLOP	119
Qy	117	AEKDKKGLPLTRCVRFFISPEKKLAASILYPATTGRNFAEILRLVLDLSQLTAKFPVATPV	176
Db	120	AEKDEKMPVTAUVVFVCGPKDKLKLILYPATTGRNFDDELRLVVISLQITAEKRVATPV	179
Qy	177	DWTAGAKCCVVPNLAAEAQRLLLPKGHEALQLPSGKPYLRLTPDP	221
Db	180	DWKDGSVMVLPTPIEEAKKLPFGVFTKSLPSGKKYLRVTPOP	224

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RESULT 15
US-10-205-823-198
; Sequence 198, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-198

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[illegible]

RESULT 17
US-10-502-279-8
Sequence 8, Application US/10502279
Publication No. US2005008480A1
GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
APPLICANT: Hideki ENDOH
APPLICANT: Ryosuke NAKANO
APPLICANT: Eiji KUROSAKI
APPLICANT: Miyuki KATO
APPLICANT: Hiroyuki YOKOTA
APPLICANT: Kazumori INABE
TITLE OF INVENTION: METHOD FOR SCREENING A DRUG AMELIORATING INSULIN RESISTANCE
FILE REFERENCE: 082704
CURRENT APPLICATION NUMBER: US/10/502,279
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: JP 2002-013721
PRIOR FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: JP 2002-257703
PRIOR FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 224
TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-502-279-8

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDFAEALGAHRLHEYLGDSDGVMFSDHNDFTPVCTTELAEAVKLD 58
DB 1 MFGGLLLGDVAPNEFANTT-VGRIRFHDFLGDSGILFSDHNDFTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKIDMAY--AGRSNLPPLVCDPNRELAASIGIMDP 116
DB 60 EFARNVKLIATLSIDSVEDHLAWSKDINAYNCEBTEKLPFPFIIDDRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPV 176
DB 120 AEKDEKGMPTARVVFVFGPKKLSILYPATTGRNFAELRLVDSLQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPKGKPYLRITPDP 221
DB 180 DWKDGSDVMVLPFTPEBAKKLPKGVFTKELPSGKKYLYRTPQP 224

RESULT 18
US-10-651-056-3
; Sequence 3, Application US/10651056
; Publication No. US20050100979A1
; GENERAL INFORMATION:
; APPLICANT: POWER, John Henry Thomas
; TITLE OF INVENTION: METHODS FOR DETECTING OXIDATIVE STRESS
; FILE REFERENCE: 0641-0254P
; CURRENT APPLICATION NUMBER: US/10/651,056
; CURRENT FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-651-056-3

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDFAEALGAHRLHEYLGDSDGVMFSDHNDFTPVCTTELAEAVKLD 58
DB 1 MFGGLLLGDVAPNEFANTT-VGRIRFHDFLGDSGILFSDHNDFTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKIDMAY--AGRSNLPPLVCDPNRELAASIGIMDP 116
DB 60 EFARNVKLIATLSIDSVEDHLAWSKDINAYNCEBTEKLPFPFIIDDRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPV 176
DB 120 AEKDEKGMPTARVVFVFGPKKLSILYPATTGRNFAELRLVDSLQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPKGKPYLRITPDP 221
DB 180 DWKDGSDVMVLPFTPEBAKKLPKGVFTKELPSGKKYLYRTPQP 224

RESULT 19
US-10-732-923-21433
; Sequence 21433, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
```

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; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21433
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-21433

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 17; Length 224;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSPPDFAEALGAHRLHEYLGDSDGVMFSDHNDFTPVCTTELAEAVKLD 58
DB 1 MFGGLLLGDVAPNEFANTT-VGRIRFHDFLGDSGILFSDHNDFTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKIDMAY--AGRSNLPPLVCDPNRELAASIGIMDP 116
DB 60 EFARNVKLIATLSIDSVEDHLAWSKDINAYNCEBTEKLPFPFIIDDRNRELAAILGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLQLTAKFPVATPV 176
DB 120 AEKDEKGMPTARVVFVFGPKKLSILYPATTGRNFAELRLVDSLQLTAKFPVATPV 179

QY 177 DWTAGAKCCVVPNLAAEAQRLPKGHEALQLPKGKPYLRITPDP 221
DB 180 DWKDGSDVMVLPFTPEBAKKLPKGVFTKELPSGKKYLYRTPQP 224

RESULT 20
US-11-051-454-198
; Sequence 198, Application US/11051454
; Publication No. US20050191673A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/11/051,454
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-454-198

Query Match
Best Local Similarity 53.5%; Score 638.5; DB 20; Length 224;
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	Best Local Similarity	55.4%; Pred. No. 1.7e-63;			
	Matches 127; Conservative	28; Mismatches 65; Indels	5; Gaps	3;	
Qy	1	MP--LNI ^{GDS} GFPDPQAEALGAEHFRLHEYL ^{GDS} SGVMFSHPENDTTPVCTTELAAEAVKLQD	58		
Dd	1	MPGGLLLGDVAPNEPANTT-VGRIRFDHFL ^{GDS} SGILFSPHRDPTPVCTTELGRAAKLAP	59		
Qy	59	SFTKKNCKLVGFSCNDLQSHREWA ^{KD} IWAY--AGRSGNLPPLVCDPNRELAAISLGIMDP	116		
Dd	60	EFAENVKLIALSIDSVDHLAWSDINAYNCBETKLPFIIDDRNELAILGLMDP	119		
Qy	117	AEDKKGLPLTCRCVFITSPBKULAA ^{SL} LYPATTTGRNPAEILRVLDSLQLTAKEFVPATPV	176		
Dd	120	AEKDEKMPVTARVVVFPGDKLKLS ^{LY} PATTGRNFDELIRVVISLQLTAEKRVA TPV	179		
Qy	177	DWTAGAKCCVVVNIAAEEAQRLPKGHEALQPSGKPYLRITPOP	221		
Dd	180	DWKDGDSVMVLTPTTPESEAKKLFPKGVFTKELPSGKKYLRVTPOP	224		

RESULT 21

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US-10-732-923-21325
; Sequence 21325, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21325
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-732-923-21325

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Query Match	53.3%	Score 636;	DB 17;	Length 220;
Best Local Similarity	55.9%;	Pred. No. 3.2e-63;		
Matches 123;	Conservative 32;	Mismatches 57;	Indels 8;	Gaps 3;
Qy	1	MPLNLGDSFPFOAEALCAEH-FRLHLEYLGSWGMFSPNDPFPVCTTCLAEAAVKLQDS	509	
Db	1	MAYHLGATFPNFTATASNVDGVDFYKVGDNWAILFSPHDPFPVCTTCLAEFGKHWE	60	
Qy	60	FTKNCKLVGSCNDLQSHREWAKDIMAYAGRSNGL----PPPLVCDPNRELAAISLIGMNP	116	
Db	61	FLKLNCKLIGPSCNSKESHDOWIEDIKFY----GNLKDWDIPMVCDSESLANQLKIMDE	116	
Qy	117	AEKDKGGLPLTRCVRFFISPSKLAASLTYPATTGRNFAEILRVLDSLQLTAKRPVATPV	176	
Db	117	KEKDIKGLPLTRCVRFFISPPKKVATVLYPATGRNSQEIIRVLKSLQLTINTHPVATPV	176	
Qy	177	DWTAGAKCCVVPNLAAEEAQRLLPKGHEALQPSGKPYLR	216	
Db	177	NWKEGDKCCIPLSDVNDAPLPLFKNEVKKLQDPSOKAYLR	216	

RESULT 22

US-10-732-923-21329
 ; Sequence 21329, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149

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; SEQ ID NO 21329
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-21329

Query Match      53.1%; Score 634.5; DB 17; Length 224;
Best Local Similarity 55.3%; Pred. NO. 4.9e-63;
Matches 125; Conservative 27; Mismatches 67; Indels 7; Gaps 4;

Qy      1  MP--LNLGDSFPDFQAE-ALGAEHFRLHEYLGDSWGMPFSHPNDPFPVCTTELAEEAVKLQ 57
      1  MPGGLLLGDEAPNFEANTTIG--RIRFHDPLGDSWGILFSPHRDFTPVCTTELGRAAKLA 58

Qy      58  DSTTKNCKVLGFSNDLQSHREWAKDIMAYAGR--SGNLPPLVCDPNRELAASLGIMD 115
      59  PEFAKRNVKLIJALISDVEDHLAWSKDINAYNGETPEKLPFPPIIDKGRDLAILLGMLD 118

Qy      116  PASEKDKKGLPLTCRCQVFFISPEKKLAASILYPATTGRNFAEIIIRVLDSLQLTAKFPVATP 175
      119  PVEKDDNNMPVTRVVFIFGPDKKLKLISLYPATTSTNFDIELIRVVDLSLQLTGCKPVATP 178

Qy      176  VDMTAGAKCCVVPNLAAEEAQRLLPKGHEALQPSGKPYRLRLTPDP 221

Qy      179  VDMKKGFESVWVFTLSEERAKOCFPPKGVFTKELPSGKKLYRLYTPOP 224

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RESULT 23

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US-10-732-923-21434
; Sequence 21434, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 21434
; LENGTH: 224
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(224)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-21434

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Query Match	52.8%;	Score 630.5;	DB 17;	Length 224;
Best Local Similarity	56.0%;	Pred. No. 1.4e-02;		
Matches	126;	Conservative 28;	Mismatches 66;	Indels 5; Gaps 3;

Qy	1	MP--LNLGDSFPDFOAEALGAEHFRLHEYLGDSWGVMFSPNDFTFPVCTTTELAEAVKLQD	58
Db	1	MPGGLLLGDVAPNFEAINT--VGRIRFHFDFLGDSWGILFSPRDFTPVXTTTELGRAAKLAP	59
Qy	59	SFTKCKNKLVGFSNCNDLQSHREWAKOIMAYAGR--SGNLPFLVCDNRNLEAASLGIMDP	116
Db	60	EFAKRNKKLLALSIDSVEDHSAWSKOINAYNSEPTKELFPFIIDRRNLEAILLGLMDP	119
Qy	117	AEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSLOQTAKFPVPATPV	176
Db	120	AEKDEKMPYARVVFVGGDKKLKLSILYPATTGRNFDEILRVVLSLOLTAEKRVATPV	179
Qy	177	DWTAGAKCCVVPNLAAEEAQRLLPKGHEALQLPSGKPYRLTDPD	221
Db	180	DWKDGDVSWVLPTIPBEAAKKLPKGVFTKELPSGKKLYRTQD	224

RESULT 24	US-10-732-923-21330
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0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040

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5 A-A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 21:33:02 ; Search time 167 Seconds
(without alignments)
516.452 Million cell updates/sec

Title: US-10-723-123-3
Perfect score: 1194
Sequence: 1 MPLNLGDSPPDFOAALGAE.....EALQLPSGKFLRLTDPDPRG 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1194	100.0	223	3 AAY79496	Aay79496 Elmeria t
2	669.5	56.1	225	7 ADD48548	Add48548 Rat Prote
3	669.5	56.1	225	7 ADD48997	Add48997 Rat Prote
4	668.5	56.0	223	7 ADD48552	Add48552 Rat Prote
5	668.5	56.0	223	7 ADE54680	Ade54680 Rat Prote
6	641.5	53.7	224	6 ABU07558	Abu07558 Mouse ant
7	640.5	53.6	224	2 AAW76700	Aaw76700 Mouse ant
8	640.5	53.6	224	6 ABU07559	Abu07559 Mouse ant
9	640.5	53.6	235	2 AAW88274	Aaw88274 Brugia ma
10	639.5	53.6	224	6 AAW07557	Aaw07557 Human enc
11	638.5	53.5	224	2 AAW76699	Aaw76699 Human ant
12	638.5	53.5	224	6 ADA10886	Adal0886 Human CDN
13	638.5	53.5	224	7 ADB80263	Adb80263 PPARGamma
14	638.5	53.5	224	7 ADB75374	Adb75374 Prostata
15	638.5	53.5	224	7 ADD48554	Add48554 Human Pro
16	638.5	53.5	224	8 ADO24813	Ado24813 Human per
17	638.5	53.5	224	8 ABM80206	Abm80206 Tumour-as
18	638.5	53.5	224	8 ADP23043	Adp23043 PRO polyp
19	638.5	53.5	253	4 AAW23423	Aaw23423 Novel hum
20	637.5	53.4	223	4 AAB68039	Aab68039 Amino aci
21	637.5	53.4	223	7 ADD48999	Add48999 Human Pro
22	637.5	53.4	223	7 ADE54682	Ade54682 Human Pro
23	637.5	53.4	223	7 ADD48550	Add48550 Human Pro
24	619	51.8	221	4 AAY97763	Aay97763 I. scapul
25	618.5	51.8	235	2 AAW88273	Aaw88273 Dirofilar

26	609.5	51.0	222	5 AAG66167	Aag66167 Tick pero
27	607.5	50.9	224	6 ABU07560	Abu07560 Mouse ant
28	588	49.2	222	4 ABB59626	Abb59626 Drosophil
29	585	49.0	250	2 AAR34196	Aar34196 O-CSF. 3/
30	507.5	42.5	177	8 ADO24814	Ado24814 Human per
31	507.5	42.5	212	8 ADS24874	Ads24874 Bacterial
32	501.5	42.0	220	4 ABB65897	Abb65897 Drosophil
33	498.5	41.8	220	4 ABB59059	Abb59059 Drosophil
34	497.5	41.7	222	7 ABO68070	AbO68070 Pseudomon
35	495	41.5	218	5 ABB80958	Abb80958 Barley 1-
36	494.5	41.4	212	8 ADN21975	Adn21975 Bacterial
37	494.5	41.4	212	8 ADN24733	Adn24733 Bacterial
38	494.5	41.4	216	6 ADA34041	Ada34041 Acinetoba
39	493.5	41.3	212	8 ADN22014	Adn22014 Bacterial
40	493.5	41.3	212	8 ADN24773	Adn24773 Bacterial
41	492	41.2	211	8 ADN20019	Adn20019 Bacterial
42	486.5	40.7	216	5 ABB80959	Abb80959 A. thalia
43	486.5	40.7	216	6 ABR39572	Abr39572 A. thalia
44	481	40.3	211	8 ADS21318	Ads21318 Bacterial
45	473.5	39.7	212	8 ADN26021	Adn26021 Bacterial

ALIGNMENTS

RESULT 1
AAY79496
ID AAY79496 standard; protein; 223 AA.
XX AC
XX AAY79496;
XX XX
DT 01-AUG-2000 (first entry)
XX XX
DE Elmeria tenella 25 kDa peroxidoxin-like hydrophilic protein.
XX XX
KW Coccidiosis; vaccine; poultry; peroxidoxin.
XX XX
OS Elmeria tenella.
XX XX
PN EP995799-A2.
XX XX
PD 26-APR-2000.
XX XX
PF 01-OCT-1999; 99EP-00203214.
XX XX
PR 07-OCT-1998; 98EP-00203384.
PR 16-OCT-1998; 98EP-00203457.
XX XX
(ALKU) AKZO NOBEL NV.
XX XX
PI Schaap TC, Kuijper CM, Vermeulen AN;
XX XX
DR WPI; 2000-305655/27.
N-PSDB; AAZ294936.
XX XX
PT Novel hydrophilic Elmeria polypeptides comprise sequences with at least
70% homology with sequences of 13-223 amino acids, useful as vaccines
against Coccidiosis in poultry.
XX XX
PS Claim 3; Page 3; 30pp; English.
XX XX
CC The present sequence is that of a 25 kDa peroxidoxin-like hydrophilic
protein of Elmeria tenella. The polypeptide was obtained from the
hydrophilic phase of a total sporozoite protein fraction of E. tenella
weybridge strain. The invention provides 6 hydrophilic polypeptides (see
AA79494-99) of Elmeria. These polypeptides, or immunogenic fragments of
them, can be used in vaccines to protect poultry against the pathogenic
effects of Elmeria, the causative agent of intestinal coccidiosis. The
polypeptides are also useful for detecting antibodies against Elmeria
infection in poultry. DNA encoding the polypeptides can be used to detect
Elmeria parasites and as a vaccine, optionally in a live recombinant
carrier

Db 7 LGDKFPDQAESESSIFSHDWGKDSMAILFSHPDRDFTVCTTELARLVLEPEFKR 66
Qy 64 NCKLVGFSNCDLQSHREWAKDIMAYGR-----SGN-LPPLVCDPNRELAASIGI 113
Db 67 NVKLIGLSCDSVQSHRWADDIIFELCRKSGDSNTCCSGNKLPPPIIADNRSLASKLGM 126
Qy 114 MDPAEKDKGLPLTCRCVFFISPBKLAASILYPATTGRNFAELRLVDSLSQLTAKFPVA 173
Db 127 MDPDECDEKGAALTARCLFTIGPEKTLKLSILYPATTGRNFDILRVVDSLSQLTATKVA 186
Qy 174 TPVDWTAGKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYLRITPDP 222
Db 187 TPVDWQMGDDCVVPTINDNEAKLFGKINTVELPSGKPYLRVWAHPK 235

RESULT 10
ABU07557
ID ABU07557 standard; protein; 224 AA.
XX AC ABU07557;
XX 18-MAR-2003 (first entry)
XX Human encoding antioxidant protein 2, Aop2.
DE Human; antioxidant protein 2; Aop2; atherosclerosis; antiatherosclerotic;
KW antioxidant; atherosclerotic lesion; oxidative damage; heart surgery;
KW chromosome 1q23-25.
XX Homo sapiens.
XX

Key Location/Qualifiers
FT Misc-difference 1..224
FT /note= "The last letter of the last Amino acid in each
FT row has not been reproduced in the specification, the
FT index has added the correct letter to restore the
FT correct 3 letter code except where ambiguity exists (see
FT below)"
FT Misc-difference 96
FT /label= OTHER
FT /note= "Encoded by GAA, probably Glu, appears as Gl in
FT the specification"
XX

US2002142417-A1.
XX
XX 03-OCT-2002.
XX
XX 28-MAR-2001; 2001US-00819505.
XX
XX 02-APR-1997; 97US-0040898P.
XX 01-APR-1998; 98US-00053088.
XX
XX (PAIG/) PAIGEN B.
XX (BEIE/) BEIER D R.
XX
XX Paigen B, Beier DR;
XX
XX WPI; 2003-155944/15.
XX N-PSDB; ABX15201.
XX

Novel antioxidant protein-2 polypeptide useful for diagnosing
predisposition to atherosclerotic lesions in subject, and screening a
compound for the protein stimulatory activity.
XX
XX Claim 4; Page 38; 54pp; English.
XX

The invention relates to an isolated antioxidant protein-2 polypeptide,
designated Aop2, its antigenic fragment or the nucleotide encoding Aop2
(Aop2 NA). Also included are Aop2 NA oligonucleotides, screening a
compound for Aop2 stimulatory activity, screening a compound for anti-
atherosclerotic activity (by providing a lipid, contacting the lipid with
a candidate antioxidant, and determining the oxidation state of the
lipid), an anti-Aop2 mono/polyclonal antibody, an Aop2 NA expression

CC vector, a host cell comprising Aop2 NA and reducing atherosclerotic
CC lesions in a subject (by administering a lipid antioxidant composition to
CC the subject). Aop2 is useful for diagnosing a predisposition to
CC atherosclerotic lesions in a subject involving determining the
CC antioxidant activity of an Aop2 polypeptide of the sample, or the level
CC of an Aop2 polypeptide in cells of the sample or involves polymerase
CC chain reaction (PCR), and the determining step is performed by contacting
CC the sample with an anti-Aop2 antibody, or determining the sequence of
CC nucleic acid from the sample that encodes an Aop2 polypeptide. Aop2 is
CC also useful for screening a compound for Aop2 stimulatory activity. Aop2
CC NA is useful for increasing Aop2 function in a cell. The expression
CC vector may be a viral vector, encapsulated in a liposome. The viral
CC vector is adenoviral, retroviral, vaccinia, adeno-associated viral
CC vector, or herpes viral vector. The cell is located in a human subject,
CC or an experimental animal. The promoter is cytomegalovirus (CMV), rous
CC sarcoma virus (RSV), or E1A. Aop2 is also useful in preventing oxidative
CC damage in vivo, for e.g., during heart surgery, where blood is oxygenated
CC outside the body. Aop2 or Aop2 NA is useful for treating atherosclerosis.
CC The present sequence represents human Aop2, the gene for which is located
CC on human chromosome 1q23-25
XX
SQ Sequence 224 AA;

Query Match 53.6%; Score 639.5; DB 6; Length 224;
Best Local Similarity 56.4%; Pred. No. 3.2e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

Qy 1 MP--LNLGSPDFQAEALGAEHFRLEHVLGDSWGMFSPNDFTVCTTELEAVKLQD 58
Db 1 MPGLLLGDVAPNFEANTT-VGRIRPHDFLGDWSGLFSHPDRDFTVCTTELGRAAKIAP 59
Qy 59 SPTKKNCKLVGFSNCDLQSHREWAKDIMAY--AGRSNLPFPVLVCDPNRELAASLGIMDP 116
Db 60 EFAKRVKLIALLSIDSVEDEHLAWSKDINAYNCEPTXKLPFFIIDRNLAILLGLMDP 119
Qy 117 AEKDKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVDSLSQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGPKKLSILYPATTGRNFDILRVVDSLSQLTAEKRVATPV 179
Qy 177 DWTAGKCCVVPNLAABEAQRLLPKGHEALQLPSGKPYLRITPDP 221
Db 180 DWKGDGSMVLPFTIPEEAKKLPFGVFTKELPSGKKYLRYPQP 224

RESULT 11
AAW76699
ID AAW76699 standard; protein; 224 AA.
XX AC AAW76699;
XX
XX 02-FEB-1999 (first entry)
XX
XX Human antioxidant protein 2 (AOP2).
XX
XX Antioxidant protein 2; AOP2; human; atherosclerosis; Acl1; heart disease;
KW diagnosis; therapy; drug screening.
XX
XX Homo sapiens.
XX
XX WO9843666-A1.
XX
XX 08-OCT-1998.
XX
XX 01-APR-1998; 98WO-US006666.
XX
XX 02-APR-1997; 97US-0040897P.
XX
XX (JACK-) JACKSON LAB.
XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
XX Paigen B, Beier DR;
XX
XX WPI; 1998-568267/48.
XX
XX

PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; NP_004896.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 224 AA;

Query Match 53.5%; Score 638.5; DB 7; Length 224;
Best Local Similarity 56.4%; Pred. No. 4.1e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSFPDFOAEALGAHFLHLYLGDGSGVMFSDHPNDFTPVCTTELAEAVKLQD 58
Db 1 MPGGLLLGDVAPNFEANTT-VGRIRHDFLGDGSGILFSDHPNDFTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPFPLVCDPNRELAASLGIMDP 116
Db 60 EFAKRNVLKIALSIDSVEDHLAWSKDINAYNCEPTEKLPFPFIIDRRNELAILLGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLSLQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGDPDKKLKLSILYPATTGRNFDLRLVLSLQLTAEKRVATPV 179

QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYRLRLTPDP 221
Db 180 DWKDGDSVMVLPITPEEAKKLFPKGVFTKELPSGKKLYRLTPQP 224

RESULT 16
ADO24813
ID ADO24813 standard; protein; 224 AA.

XX ADO24813;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human peroxiredoxin IV protein.
XX
XX vulnary; anti-oxidant; free radical; peroxiredoxin; dihydroliipoic acid;
KW radiation burns; thermal burns; chemical burns; enzyme.
XX
OS Homo sapiens.
XX
PN WO2004043485-A1.
XX
PD 27-MAY-2004.
XX
XX 05-NOV-2003; 2003WO-RU000473.
XX
PR 10-NOV-2002; 2002RU-00129774.
PR 29-JUL-2003; 2003RU-00123534.
XX
PA (ASCE=) AS RUSSIA INST CELL BIOPHYSICS.
XX
PI Fesenko EE, Novoselov VI, Yanin VA, Lipkin VM, Shuvaeva TM;
XX
XX WPI; 2004-420104/39.
DR N-P8DB; ADO24807.
XX
PT Composition for the antioxidant protection of cells, tissues and whole
PT organisms comprises a peroxiredoxin polypeptide, a peroxiredoxin fragment
PT and/or dihydroliipoic acid.
XX
PS Claim 8; SEQ ID NO 1; 62pp; Russian.
XX
CC The invention relates to a pharmaceutical composition for the antioxidant
CC protection of cells, tissues and whole organisms against hyperproduction
CC of free radicals comprising a peroxiredoxin polypeptide, a peroxiredoxin
CC fragment and/or dihydroliipoic acid in a total amount of 10-90 wt.%. The
CC composition is useful for treating disorders caused by an imbalance
CC between oxidative and reductive processes in mammalian organisms and
CC cells, e.g. to treat the effects of radiation, thermal and chemical burns
CC and injuries caused by disasters and fires. This sequence corresponds to
CC the human peroxiredoxin IV protein.
XX
SQ Sequence 224 AA;

Query Match 53.5%; Score 638.5; DB 8; Length 224;
Best Local Similarity 56.4%; Pred. No. 4.1e-63;
Matches 127; Conservative 28; Mismatches 65; Indels 5; Gaps 3;

QY 1 MP--LNLGDSFPDFOAEALGAHFLHLYLGDGSGVMFSDHPNDFTPVCTTELAEAVKLQD 58
Db 1 MPGGLLLGDVAPNFEANTT-VGRIRHDFLGDGSGILFSDHPNDFTPVCTTELGRAAKLAP 59

QY 59 SFTKKNCKLVGFSNDLQSHREWAKDIMAY--AGRSNLPFPLVCDPNRELAASLGIMDP 116
Db 60 EFAKRNVLKIALSIDSVEDHLAWSKDINAYNCEPTEKLPFPFIIDRRNELAILLGLMDP 119

QY 117 AEKDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRLVLSLQLTAKFPVATPV 176
Db 120 AEKDEKGMPTARVVFVFGDPDKKLKLSILYPATTGRNFDLRLVLSLQLTAEKRVATPV 179

QY 177 DWTAGAKCCVVPNLAEEAQRLLPKGHEALQLPSPGKPYRLRLTPDP 221
Db 180 DWKDGDSVMVLPITPEEAKKLFPKGVFTKELPSGKKLYRLTPQP 224

RESULT 17
ABM80206
ID ABM80206 standard; protein; 224 AA.
XX
AC ABM80206;
XX

XX	SQ	Sequence 224 AA;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
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	Best Local Similarity	56.6%;	Pred. No. 5.3e-63;			
	Matches	125;	Conservative	28;	Mismatches	65;
					Indels	3;
						Gaps
						2
QY	3	NLGDSPFD	QOAEALGA	EHFLHLYGLD	SGVMFSEHNDETPVCTT	ELAEAVKLQDSFTK
Db	4	LULGDVAPN	FEANTT	-VGRIRFHD	PLDGSWGILFSHPDRDTPVCTT	ELGRAAKLAPEFAK
QY	63	KNCKLVG	SCNDLQ	SHREAWKIDWAY	-AGRSGNLP	PLPCLVDNRRELAA
Db	63	RNVKLIAL	SIDS	VEDHLAWSKDINAYN	CEBTEKLP	PIIDDRRELAILGLMDPAEK
QY	121	KKGLPLT	CRCVFFTS	PEKKLAASILYPAT	TGRNPAEILRVLD	SLQUTAKFPVATPV
Db	123	BKGMVPT	ARVVVFV	FGDDKKLSILYPAT	TGRNFEILRVVILQUT	AKERVATPV
QY	181	GAKCCV	WPNLAAEEA	QRLLPKGHEALQ	LPSCGPYIRL	TPDP
Db	183	GDSVMVL	PTPIEEEA	KKLPFGKGVFTK	LPSCGKYLRV	TPDP

RESULT 21	
ADD48999	
ID	ADD48999 standard; protein; 223 AA.
XX	
AC	ADD48999;
XX	
DT	02-DEC-2004 (revised)
DT	29-JAN-2004 (first entry)
XX	
DE	Human Protein P30041, SEQ ID NO 14711.
XX	
DE	Human; pain; neuronal tissue; gene therapy;
XX	
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
KW	spared nerve injury; SNI; Chung.
XX	
OS	Homo sapiens.
OS	Unidentified.
XX	
PN	WO2003016475-A2.
XX	
PD	27-FEB-2003.
XX	
PF	14-AUG-2002; 2002WO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P.
PR	01-NOV-2001; 2001US-0346382P.
PR	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GEHO) GEN HOSPITAL CORP.
PA	(FARB) BAYER AG.
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M;
XX	
DR	WPI; 2003-268312/26.
DR	GENBANK; P30041.
XX	
PT	New composition comprising two or more isolated polypeptides, useful for
PT	preparing a medicament for treating pain in an animal.
XX	
PS	Example 1; Page; 1017pp; English.

compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://pub.int/pub/published/pct/sequences).

Query Match	53.4%	Score	637.5	DB	7	Length	223
Best Local Similarity	56.6%	Pred. No.	5.3e-63				
Matches	125	Conservative	28	Mismatches	65	Indels	3
Gaps	2						

Qy	3	LNIGDSDPDFOAELGAEHFRLEHYIGDSWGMFSGHPNDFTPVCTTELAEAVKLQDSFTK	62
Db	4	LLIGDVAPNEANTT-VGRIRFDFGLDSWGILFSHPRDFTPVCTTELGRAKLAPFAK	62
Qy	63	KNCKLVGFGSNDLQSHREWAKIMAY--AGRSGNLPPLVCDPNRELAAASLGIMDPAEKD	120
Db	63	RNVKLIALSIDSVEDHLAWSKDINAYNCEBTEKLPFPDIIDRNRELAILGLMLDPAEKD	122
Qy	121	KGGLPLTRCVCVFFISPEKKLAASILYPATTCGRNFAEILRLVDSLQLTAKFPVATPVDTWA	180
Db	123	EKGMPVTARVVVFGPDKKLKSILYPATTCGRNDEILRLVISLQLTAEKRVATPVDDWKD	182
Qy	181	GAKCCVVPNLAAEBAQRLLPKGHEALQLPSGKPYLRLLTPDP	221
Db	183	GDSVWVLPTPIPEEBAKKLFPGKGVFTKELPSGKPYLRYPQP	223

RESULT 22	
AE4S4682	
ID	AE4S4682 standard; protein; 223 AA.
XX	
AC	AE4S4682;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human Protein P30041, SEQ ID NO 487.
XX	
KW	Human; pain; neuronal tissue; gene therapy;
KW	spinal segmental nerve injury; chronic constriction injury; CCI;
KW	scared nerve injury; SNI; Chung.

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
XX Example 1; Page; 1017pp; English.
PS
PS
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at <http://wipo.int/pub/published/pct> sequences.

Sequence 223 AA;

ry Match	53.48;	Score	637.5;	DB	7;	Length	223;	
t Local Similarity	56.68;	Pred. No.	5.3e-63;					
ches 125;	Conservative	28;	Mismatches	65;	Indels	3;	Gaps	2;

3	LNLGDSFPDQAEALGAEGHRLHEYLGDLSGVMFSPHNDEFTPVCTTTELAAVKLQDSFTK	62
4	LLLGDVAPNEANTT-VGRIRFHDFLGDSMGILFSPHRDFTPVCTTELGRAAKLAPEFAK	62
63	KNCKLVCFSCNDLOSHREWAKDIWAY--AGRSGNLPPFLVCDPNRELAASLGIMDPAEKD	120
63	RNVKLIALLSIDSVEDHLAWSKDINAYNCBPTKLPFFIIDRRNRELAIIILGMLDPAEKD	122
121	KKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELIRLVLDLSQLTAKFPVATPVDTWA	180
123	EKGMPVTARVVVFPGDKKLKLSILYPATTGRNFEDELVRVVISQLTAEKRVATPVDKD	182
181	GAKCCVVPNLAAEBAQRLPKGHEALQLPSGKPYRLRTPDP	221
183	GDSVWVLPTTPIEEBAKLLFKPGVFTKELPSGKKYLRYTPQP	223

RESULT 23

ADD48550

ID ADD48550 standard; protein; 223 AA.

AC ADD48550:

XXXX

DT 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Human Protein P30041, SEQ ID NO 14254.

XV Human: origin, development, evolution.

KW spinal segment; human; path; segment

kw spared nerve
kw spared nerve

XX
PN WO2003016475-A2.

27-FEB-2003

14-AUG-2002: 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033334
YY

PA (GEHO) GEN HOSPT

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso

XX
DR WPI; 2003-268312/26.
DR GENBANK; P30041.
XX
XX PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

Example 1: page: 1017pp: English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIP0 at ftp.wipo.int/pub/published/pct sequences.

Sequence 223 AA:

Query Match	53.4%;	Score	637.5;	DB	7;	Length	223;
Best Local Similarity	56.6%;	Pred. No.	5.3e-63;				
Matches	125;	Conservative	28;	Mismatches	65;	Indels	3;
Gaps	2;						
QY	3	LNIGDSFPDQAEALGAEHFRLHEYLGDSGWMFMSHPNDFTPVCTTELAAVAKLQDSFTK	62				
DB	4	LLLGDVAPNEANTT-VGRIRHFDFLGDSWGILFESHPRDFTFPVCTTELGRAAKLAPEFAK	62				
QY	63	KNCKLVGFSNDLQSHREWAKOIMAY--AGRSGNLFPFLVCDPNRELAASLGIMDPAEKD	120				
DB	63	RNVKLIALSDSVEDHLAWSKOINAYNCBETPKLPPIIDDRNRELAILLGMIDPAEKD	122				
QY	121	KKGLPLTCTRCVPFISPEKKLAASILYPATTGRNFAETLRVLDSLQLTAKPPVATPVDDWTA	180				
DB	123	EKGMPVATRVVFGDPKKLKULYPATTGRNFDILRVVISLQLTAKRVATPVDDWK	182				
QY	181	GAKCCVVPNLAAEAEQRLLPKGEALQLPFSKGKPYLRLTDPD	221				
DB	183	GDSVMVLPTIPREEAKKLPKGVFTKELPSGKKLYRVTOP	223				

RESULT 24
AA97763
ID AAY97763 standard; protein; 221 AA.
XX AC AAY97763;
XX DT 06-AUG-2001 (first entry)
XX DE
XX DE I. scapularis Salp25C protein sequence.
XX KW Salp; tick; antibody; tick immunity; infection; tick-borne disease;
XX KW coagulation factor Xa inhibitor; inflammatory response.
XX OS Ixodes scapularis.
XX PN WO20010469-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US032765.
XX PR 03-DEC-1999; 99US-0169048P.
XX PR 16-OCT-2000; 2000US-0240716P.
XX PA (UYA) UNIV YALE.
XX PI Kantor FS, Fikrig E, Das S;
XX DR WPI; 2001-367810/38.
XX DR N-PSDB; AAA91494.
XX PT Novel Ixodes scapularis polypeptides for conferring tick immunity and for
XX PT preventing the transmission of tick-borne pathogens.
XX PS Claim 20; Fig 2; 137pp; English.
XX CC This sequence is an Ixodes scapularis polypeptide of the invention. The
XX CC proteins of the invention are 15 tick Salp proteins. The proteins, the
XX CC antibodies against them or pharmaceutical composition comprising a fusion
XX CC protein or a multimeric protein and at least one additional non-Ixodes
XX CC scapularis polypeptide, can be administered to a subject to confer tick
XX CC immunity and therefore prevent infection by a tick-borne disease.
XX CC Inhibiting coagulation factor Xa activity comprises administering to a
XX CC subject a polypeptide selected from Salp14A, Salp9A or a fragment of
XX CC these having Xa inhibiting activity, inhibiting histamine activity
XX CC comprises administering a Salp25D polypeptide or its histamine binding
XX CC fragment to a subject, and inhibiting or preventing an inflammatory
XX CC response comprises administering a polypeptide selected from a Salp15,
XX CC Salp25C, Salp13 or a fragment of these having the same activity. The
XX CC protein or its immunogenic fragment may be used to produce monoclonal
XX CC antibodies that are screened for their ability to confer tick immunity
XX CC when used to immunise naive animals. The antibody can be used to screen
XX CC for expression of I. scapularis polypeptides, either in libraries
XX CC constructed from I. scapularis nucleic acid molecules or from other
XX CC samples in which proteins may be present, and for purifying or removing
XX CC polypeptides from a given sample to block or bind to specific epitopes on
XX CC the polypeptides and to direct various molecules, such as toxins, to
XX CC ticks
XX SQ Sequence 221 AA;
Query Match 51.8%; Score 619; DB 4; Length 221;
Best Local Similarity 51.8%; Pred. No. 6.4e-61;
Matches 114; Conservative 35; Mismatches 69; Indels 2; Gaps 2;
QY 2 PLNLGSPDPFQAEALCAEHLHEYLGDWGMVFSHPNDFTPVCTTELAAVAKLQDSFT 61
DB 3 PLNLGDPFPNFTCDTTEGK-IDFHEWLGNSWGLFSHPADYTPVCTSELARAAQLHHVFQ 61
QY 62 KKNCKLVGFSNDLQSHREWAKDIMAYAG-RSGNLPPLVCDPNRELAASLGIMDPAEKD 120

DB 62 KKGVKLIALLSCDSVESHRGWIKDINAFGELPGPPYPIIADEKRDIAVKLGMLDPVEKD 121
QY 121 KKGPLPTCRCVFFISPEKKLAASIIYPATGTGRNFAEILRVLSLQLTAKFPVATPVDWTA 180
DB 122 KEGLPLTCRAVFIIGPDKMKLSMLYPATGTGRNFDVLRATDSLLVTETRKVATPAGWQK 181
QY 181 GAKCCVVPNLAAREAQRLLPKGHEALQLPSPKPYRLRLTPD 220
DB 182 GTPCMVLPSTVEEILKLPFTGIKQYEVSPGKNYLRRTMD 221
RESULT 25
AAW88273
ID AAW88273 standard; protein; 235 AA.
XX AC AAW88273;
XX DT 29-MAR-1999 (first entry)
XX DE Dirofilaria immitis thioredoxin peroxidase PDIrPx2(235).
XX KW Thioredoxin peroxidase type-2; TPx-2; PDIrPx2(235); vaccine;
XX KW anthelmintic; helminth; heartworm disease; elephantiasis; hydrocele;
XX KW therapy; diagnosis.
XX OS Dirofilaria immitis.
XX FH Key Location/Qualifiers
XX FT Active-site 49
XX PN WO9852971-A1.
XX PD 26-NOV-1998.
XX PF 21-MAY-1998; 98WO-US010474.
XX PR 23-MAY-1997; 97US-00862540.
XX PA (HESK-) HESKA CORP.
XX PA (COLS) UNIV COLORADO STATE RES FOUND.
XX PI Chandrashekar R, Tsuji N;
XX WPI; 1999-070138/06.
XX N-PSDB; AAW84203, AAW84206, AAW84208.
XX New isolated thioredoxin peroxidase type-2 nucleic acid - obtained from a
XX Dirofilaria and Brugia, used to develop products for protection against
XX parasite helminth disease such as heartworm disease.
XX Claim 10; Page 58-59; 79pp; English.
XX This polypeptide, designated PDIrPx2(823), comprises the thioredoxin
XX peroxidase type-2 (TPx-2) of Dirofilaria immitis. A cDNA clone (see
XX AAW84203) encoding the polypeptide was isolated from a D. immitis L4 cDNA
XX library on the basis of its ability to encode a protein that selectively
XX bound at least one component of immune serum from a rabbit immunised with
XX a peptide derived from a Brugia malayi transmembrane protein. The deduced
XX polypeptide shows homology to Onchocerca volvulus adult TPx protein. D.
XX immitis and B. malayi TPx-2 nucleic acid sequences (see AAW84203-14) and
XX polypeptides (see AAW88273-74) are used in vaccines (including genetic
XX vaccines, recombinant virus vaccines and recombinant cell vaccines) for
XX the protection of animals against parasite helminth disease, especially
XX heartworm disease, elephantiasis and hydrocele (claimed). They can also
XX be used for detection, diagnosis and drug screening
XX SQ Sequence 235 AA;
Query Match 51.8%; Score 618.5; DB 2; Length 235;
Best Local Similarity 54.1%; Pred. No. 8e-61;
Matches 124; Conservative 28; Mismatches 66; Indels 11; Gaps 3;
QY 5 LGDSPDFQAEALGAEHRLHEYLGDWGMVFSHPNDFTPVCTTELAAVAKLQDSFTK 63

```
Db      7 LGDKFPDFRAETWEGFIPSYDWMIGKDSWAILFESHPRDFTPVCTTELARLVQLAPBPKR 66
      ||| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      64 NCKLVGSCNDLQSHREWADIMAYAGR-----SGN-LPPFLVCDNRELAAASLGI 113
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      67 NVKLIIGLSCDSASRHRKWDDIIVAVCMKCNDDGDTCCSGNKLPPFIADENRELATELGM 126
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      114 MDPAEKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVA 173
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      127 MDPPERDENGALTARCVFIIGPEKTLKLSILYPATTGRNFDLRLRVVDSQLTAVKLA 186
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      174 TPVDWTAGKCCVVPNLAABEORLLPKGHEALQLPSGKPYRLRLTPDDR 222
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      187 TPVDMKGGDCVVLPTDDTEAKKLFGEKINTIELPSGKHYLRMVAHPK 235
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|

RESULT 26
AAG66167
ID      AAG66167 standard; protein; 222 AA.
XX      AC      AAG66167;
XX      DT      17-JUN-2002 (first entry)
XX      DE      Tick peroxidoxin (Prx) protein.
XX      KW      Peroxiredoxin; Prx; tick; vaccine; antitick agent.
XX      OS      Haemaphysalis longicornis.
XX      PN      JP2002010785-A.
XX      PD      15-JAN-2002.
XX      PF      29-JUN-2000; 2000JP-00196620.
XX      PR      29-JUN-2000; 2000JP-00196620.
XX      PA      (FARB ) BAYER KK.
XX      WPI; 2002-298337/34.
XX      N-PSDB; ABL40531.
XX      Tick peroxidoxin, a nucleic acid molecule encoding it and its use.
XX      Claim 2; Page 7; 10pp; Japanese.
XX      The invention provides a gene encoding Haemaphysalis longicornis
CC      peroxidoxin (Prx). The Prx protein can be expressed by standard
CC      recombinant methodology. The tick Prx protein and the nucleic acid can be
CC      used for a new target of tick vaccine and antitick agent. The present
CC      sequence represents the tick Prx protein
XX      SQ      Sequence 222 AA;
      Query Match      51.0%; Score 609.5; DB 5; Length 222;
      Best Local Similarity 52.3%; Pred. No. 7.6e-60;
      Matches 116; Conservative 32; Mismatches 69; Indels 5; Gaps 4;
Qy      2 PLNLGDFPDFOAE-ALGAEBHRLHLEYLGDWSGVMFSPHNDF-TPVCTTELAAVAKLQDS 59
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      3 PLNLGDFPFPNFTCETTVGTIDF--HQWLGDWSGILFSPADYTPVCTTELAAQAQLAHV 60
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      60 FTKKNCVLGVSCNDLQSHREWADIMAYAG-RSGNLPFLVCDNRELAAASLGIWDPAE 118
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      61 FAQKGVKIIALSCDSDVSHHGWTKEAFGELPDGPPFPYPIIADEKREIAVKLGLMDPVE 120
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      119 KDKKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDW 178
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Db      121 KDEGLPLTCRAVFIIGPKMKLSMLYPATTGRNFDLRLRVVDSQLTAVKLA 180
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
Qy      179 TAGAKCCVVPNLAABEORLLPKGHEALQLPSGKPYRLRLTPD 220
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
```

```
Db      181 KKGTPCMVLPSVTEBIPKLPFTGIKQYDVPSGKKYLRTMD 222
      |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:| |||:|:|
RESULT 27
ABU07560
ID      ABU07560 standard; protein; 224 AA.
XX      AC      ABU07560;
XX      DT      18-MAR-2003 (first entry)
XX      DE      Mouse antioxidant protein 2 related sequence 1.
XX      KW      Mouse; antioxidant protein 2; Aop2; atherosclerosis; antiatherosclerotic;
KW      antioxidant; atherosclerotic lesion; oxidative damage; heart surgery;
KW      Aop2-rs1.
XX      OS      Mus sp.
XX      PN      US2002142417-A1.
XX      PD      03-OCT-2002.
XX      PF      28-MAR-2001; 2001US-00819505.
XX      PR      02-APR-1997; 97US-0040898P.
XX      PR      01-APR-1998; 98US-00053088.
XX      PA      (PAIG/) PAIGEN B.
XX      PA      (BEIE/) BEIER D R.
XX      PI      Paigen B, Beier DR;
XX      WPI; 2003-155944/15.
XX      N-PSDB; ABX15216.
XX      Novel antioxidant protein-2 polypeptide useful for diagnosing
PT      predisposition to atherosclerotic lesions in subject, and screening a
PT      compound for the protein stimulatory activity.
XX      Example 8; Fig 8B; 54pp; English.
XX      The invention relates to an isolated antioxidant protein-2 polypeptide,
CC      designated Aop2, its antigenic fragment or the nucleotide encoding Aop2
CC      (Aop2 NA). Also included are Aop2 NA oligonucleotides, screening a
CC      compound for Aop2 stimulatory activity, screening a compound for anti-
CC      atherosclerotic activity (by providing a lipid, contacting the lipid with
CC      a candidate antioxidant, and determining the oxidation state of the
CC      lipid), an anti-Aop2 mono/polyclonal antibody, an Aop2 NA expression
CC      vector, a host cell comprising Aop2 NA and reducing atherosclerotic
CC      lesions in a subject (by administering a lipid antioxidant composition to
CC      the subject). Aop2 is useful for diagnosing a predisposition to
CC      atherosclerotic lesions in a subject involving determining the
CC      antioxidant activity of an Aop2 polypeptide of the sample, or the level
CC      of an Aop2 polypeptide in cells of the sample or involves polymerase
CC      chain reaction (PCR), and the determining step is performed by contacting
CC      the sample with an anti-Aop2 antibody, or determining the sequence of
CC      nucleic acid from the sample that encodes an Aop2 polypeptide. Aop2 is
CC      also useful for screening a compound for Aop2 stimulatory activity. Aop2
CC      NA is useful for increasing AOP2 function in a cell. The expression
CC      vector may be a viral vector, encapsulated in a liposome. The viral
CC      vector is adenoviral, retroviral, vaccinia, adeno-associated viral
CC      vector, or herpes viral vector. The cell is located in a human subject,
CC      or an experimental animal. The promoter is cytomegalovirus (CMV), Rous
CC      sarcoma virus (RSV), or E1A. Aop2 is also useful in preventing oxidative
CC      damage in vivo, for e.g., during heart surgery, where blood is oxygenated
CC      outside the body. Aop2 or Aop2 NA is useful for treating atherosclerosis.
CC      The present sequence represents mouse Aop2-rs1, Aop2 related sequence 1
XX      SQ      Sequence 224 AA;
      Query Match      50.9%; Score 607.5; DB 6; Length 224;
      Best Local Similarity 52.7%; Pred. No. 1.3e-59;
```

Matches 119; Conservative 32; Mismatches 68; Indels 7; Gaps 4;

QY 1 MP--LNLGDSFPDQAE-ALGABHRLHEYLGDWGMFSPHNDFTPVCTTELAEAVKLQ 57
 DB 1 MPGLLGEAPDPEANTTIG--RIRFHDFLGNWGLFSPKDFTPVCTTELGRAAKLA 58
 QY 58 DSFTKCKLVGSCNDLQSHREWAKDIMAYAGRS--GNLPEPLVCDPNRELAASLGIMD 115
 DB 59 PEFKRNKVLIALUSVSDVHDLAWSKDINAYGATPKKLPFPPIIDDKORDISILFCMJD 118
 QY 116 PAEKDKKGLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATP 175
 DB 119 PVEKDANSPLTARGVIFGPKDKLWMLLYPNSTGRNFDLIRVIDSLQLTETKPVATP 178
 QY 176 VDMTAGAKCCVNPVLAABEAQRLLPKGHEALQLPSGKPYRLRTPDP 221
 DB 179 VDWKKGESVMVLPDLPEEAKRFPKPGIGSTTKLPKSGKNVLRYPQP 224

RESULT 28
 ABB59626
 ID ABB59626 standard; protein; 222 AA.
 XX
 AC ABB59626;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 5670.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL03729.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 5670; 21pp + Sequence Listing; English.
 CC
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 222 AA;

Query Match 49.2%; Score 588; DB 4; Length 222;
 Best Local Similarity 49.3%; Pred. No. 2e-57;
 Matches 108; Conservative 38; Mismatches 71; Indels 2; Gaps 2;

QY 3 LNLGDSFPDQAEALGABHRLHEYLGDWGMFSPHNDFTPVCTTELAEAVKLQDSFTK 62
 DB 6 LNLGDSFPDQAEALGABHRLHEYLGDWGMFSPHNDFTPVCTTELAEAVKLQDSFTK 64
 QY 63 KCKLVGSCNDLQSHREWAKDIMAYAGRSGNLPPFLVCDPNRELAASLGIMDPAEKOKK 122
 DB 65 RGVKPIALSCDVFESHKGWIEDIKSF-GKLSDFDPIADDKRELAKENMLDKOBINAE 123
 QY 123 GLPLTCRCVFFTSPEKKLAASILYPATTGRNFAEILRVLDLSQLTAKFPVATPVDMTGA 182
 DB 124 GIPLTCRAVFVVDKDKLRLSLYPATTGRNFDLIRVIDSLQLTQTKSVATPADWKQGG 183
 QY 183 KCCVNPVLAABEAQRLLPKGHEALQLPSGKPYRLRTPDP 221
 DB 184 KCVLPFTVKAEDVPKLPDPDGIETIELPSGKSYLRITPQP 222

RESULT 29
 AAR34196
 ID AAR34196 standard; protein; 250 AA.
 XX
 AC AAR34196;
 DT 25-MAR-2003 (revised)
 DT 04-AUG-1993 (first entry)
 XX
 DE O-CSF.
 XX
 KW Osteoclast colony stimulating factor; O-CSF; hypercalcaemia; inducing;
 KW murine; mammary; tumour; tetracycline-resistant acid phosphatase; TRAP;
 KW progenitor; bone marrow; SDS-PAGE.
 XX
 OS Mus musculus.
 XX
 PN WO9307271-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 30-SEP-1992; 92WO-US008322.
 XX
 PR 01-OCT-1991; 91US-00770042.
 XX
 PA (WASH-) WASHINGTON RES FOUND.
 XX
 PI Lee MY, Osborne WRA, Eyre DR;
 XX
 DR WPI; 1993-134460/16.
 DR N-PSDB; AAQ38837.
 XX
 PT New osteoclast colony stimulating factor - induces osteoclast
 PT progenitor(s) for differentiation and proliferation from bone marrow for
 PT treatment of eg. osteopetrosis.
 XX
 PS Claim 13; Fig 15; 59pp; English.

CC This sequence represents osteoclast colony stimulating factor (O-CSF)
 CC which was isolated from conditioned medium of a hypercalcaemia-inducing
 CC murine mammary tumour. O-CSF protein is capable of stimulating growth of
 CC tetracycline-resistant acid phosphatase (TRAP)-positive osteoclast progenitors
 CC in bone marrow cell cultures. O-CSF has an apparent molecular weight of
 CC approx. 15-25 kD, with a peak of biological activity at approx. 20 kD, as
 CC determined by SDS-PAGE and biological assay. The O-CSF protein may be
 CC purified from the culture medium of CESJ-3 cells and has an osteoclast
 CC progenitor stimulating activity of at least 660,000 U/mg. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 250 AA;

Query Match 49.0%; Score 585; DB 2; Length 250;
 Best Local Similarity 53.5%; Pred. No. 5.3e-57;
 Matches 116; Conservative 29; Mismatches 64; Indels 8; Gaps 4;
 QY 6 GDSFPDQAE-ALGABHRLHEYLGDWGMFSPHNDFTPVCTTELAEAVKLQDSFTKKN 64

Db 1 GDEAPNEANTTIG--RIRFHDPLGDSWGLFSPDRDFTPVCTTELGRAAKLAPEFAKRN 58
QY 65 CKLVGFCNDLQSHREWAKOIMAYGR--SGNLPPLVCDPNRELAASLGTMDBAEKDKK 122
Db 59 VKLTALSIDSVEDHLAWSKOINAYNGETPEKLPFPPIIDDKGRDLAILGLMLDVPQKDDN 118
QY 123 GLPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVPVATPDVDTAGA 182
Db 119 NMPVTARVVFIFGPKDKLKLILYPATTGRNFDILRVLDLSQLTGTGKPVATPDVVKGE 178
QY 183 KCCVVPNLAEEAQRLLPKGHEALQLPSGKPYLRLTP 219
Db 179 SVMVPTLSLEEARQCFKPGVFTKELPSGK---KLPP 212

RESULT 30

ADO24814
ID ADO24814 standard; protein; 177 AA.

XX AC ADO24814;
XX DT 12-AUG-2004 (first entry)
XX XX

DE Human peroxiredoxin IV protein N-terminal fragment.

XX vulnerable; anti-oxidant; free radical; peroxiredoxin; dihydroliipoic acid;
XX radiation burns; thermal burns; chemical burns; enzyme.

XX Homo sapiens.

XX WO2004043485-A1.

XX 27-MAY-2004.

XX 05-NOV-2003; 2003WO-RU000473.

XX 10-NOV-2002; 2002RU-00129774.

XX 29-JUL-2003; 2003RU-00123534.

XX (ASCE=) AS RUSSIA INST CELL BIOPHYSICS.

XX Feenko EE, Novoselov VI, Yanin VA, Lipkin VM, Shuvaeva TM;

XX WPI; 2004-420104/39.

XX N-PSDB; ADO24808.

XX Composition for the antioxidant protection of cells, tissues and whole
PT organisms comprises a peroxiredoxin polypeptide, a peroxylredoxin fragment
PT and/or dihydroliipoic acid.

XX Claim 8; SEQ ID NO 2; 62pp; Russian.

XX The invention relates to a pharmaceutical composition for the antioxidant
CC protection of cells, tissues and whole organisms against hyperproduction
CC of free radicals comprising a peroxiredoxin polypeptide, a peroxylredoxin
CC fragment and/or dihydroliipoic acid in a total amount of 10-90 wt.%. The
CC composition is useful for treating disorders caused by an imbalance
CC between oxidative and reductive processes in mammalian organisms and
CC cells, e.g. to treat the effects of radiation, thermal and chemical burns
CC and injuries caused by disasters and fires. This sequence corresponds to
CC the N-terminal fragment of the human peroxiredoxin IV protein.

XX SQ Sequence 177 AA;

Query Match 42.5%; Score 507.5; DB 8; Length 177;
Best Local Similarity 57.3%; Pred. No. 1.8e-46;
Matches 102; Conservative 23; Mismatches 48; Indels 5; Gaps 3;

QY 1 MP--LNLGDSFPDQAEALGAEHRLHEYLGDSWGVFSPNDPTPVCTTELEAVKLQD 58

Db 1 MPGLLLGDVAPNFEANTT-VGRIRFRDFLGDWSGILFSPDRDFTPVCTTELGRAAKLAP 59

QY 59 SFTKXKNCVLGFSFSCNDLQSHREWAKOIMAY--AGRSNLPPLVCDPNRELAASLGIMDP 116
Db 60 EFAKRVKLIALSIDSVEDHLAWSKOINAYNCEPTEKLPFPPIIDDRNRELAAILGLWLD 119
QY 117 AEKDKKGLPLTCTRCVFFISPEKKLAASILYPATTGRNFABILRVLDLSQLTAKFPVPVAT 174
Db 120 AEKDEKGMPTARVVFVFGPKDKLKLILYPATTGRNFDILRVLDLSQLTAKRVAT 177

RESULT 31

ADS24874
ID ADS24874 standard; protein; 212 AA.

XX AC ADS24874;

XX DT 02-DEC-2004 (first entry)

XX Bacterial polypeptide #13907.

XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOV/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 13907; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 212 AA;

Query Match 42.5%; Score 507.5; DB 8; Length 212;
Best Local Similarity 47.3%; Pred. No. 2.3e-48;
Matches 105; Conservative 34; Mismatches 70; Indels 13; Gaps 5;
QY 1 MPLNLGDSFPDFOAEALGAEHFRLHEYLGDWSGMFSPNDFTPVCTTELAEAVKLQDSF 60
Db 1 MSRLGDIADFPQDS-SAGKIRFHEWLGDWSGLFSPADFTPVCTTELGFATAKURDF 59
QY 61 TKXNCKLVGFCNDLQSHREWAKDIMAYAGRSNLPPLVCDPNRELAASLGIMDPAEKD 120
Db 60 TKGVAIALSVDPVDSHHKWIEDINETQNTIVN--FPILADADRVSDLYLIHPNAND 117
QY 121 KGLPLTCRCVFFISPEKKLAASILYPATTGRNPAEILRLVLDLSQLTAKFPVATPVVDWTA 180
Db 118 ----TLTVRSLFVIDPNKKRLITITYPASTGRNFHEILRLVIDLSQLTDNYKVATPANWQD 173
QY 181 GAKCCVVPNLAAE-EAQRLLPKGHEALQLPSGPKPYLRLTDP 221
Db 174 GEEVIVPSLKDEDEIKQRFPGKTRAV-----KPYLRLTQOP 210

RESULT 33
ABB65897
ID ABB65897 standard; protein; 220 AA.
XX
AC ABB65897;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 24483.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL10000.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 24483; 2lpp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 220 AA;
Query Match 42.0%; Score 501.5; DB 4; Length 220;
Best Local Similarity 44.5%; Pred. No. 1.2e-47;
Matches 97; Conservative 39; Mismatches 79; Indels 3; Gaps 3;
QY 3 LNLGDSFPDFOAEALGAEHFRLHEYLGDWSGMFSPNDFTPVCTTELAEAVKLQDSFTK 62
Db 1 MRLGQTVPNFEADTTKGP-IKPHMQGNSMVLVFSHPADFTPVCTTELGRIVAHQPEFAK 59
QY 63 KNCKLVGFCNDLQSHREWAKDIMAYA-GRSNLPPPLVCDPNRELAASLGIMDPAEKDK 121
Db 60 RNTKCLAHSDVALNSHVDWVNDIKSYCLDIPGDFPYPIIADPTDRDLAVSLGLMDERQKKD 119
QY 122 KGLPLTCRCVFFISPEKKLAASILYPATTGRNPAEILRLVLDLSQLTAKFP-VATPVVDWTA 180
Db 120 PEVGKTIRALFTISPDHKVRLSMFYPMSTGRNVDEILRTIDSQLTDLRLKVVATPANWTP 179
QY 181 GAKCCVVPNLAAEAEQRLLPKGHEALQLPSGPKPYLRLT 218
Db 180 GTKWMLPTVTDDEAHKLPFGDKVSMPSGVNYVRTT 217
RESULT 33
ABB59059
ID ABB59059 standard; protein; 220 AA.
XX
AC ABB59059;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 3969.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
XX
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL03162.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 3969; 2lpp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 220 AA;
Query Match 41.8%; Score 498.5; DB 4; Length 220;
Best Local Similarity 44.0%; Pred. No. 2.5e-47;
Matches 96; Conservative 40; Mismatches 79; Indels 3; Gaps 3;
Qy 3 LNLGDSPPDFOAEALGAHFRHLYLGDGSGWVMSFHPNDFTPVCTTTELAELAVKLDQSF 62
Db 1 MRLGOTVNFPEADTTKGP- IKFHEWQGNWVWVLSFHPADFTPVCTTTELGRIAVHQPEFAK 59
Qy 63 KNCVLGFSNDLQSHREWAKDIWAYA-GRSGNLPFLVCDPNRELAASLGIMDPAEKD 121
Db 60 RNTKCLAHSDALNSHDVNDWIKSYCLDIPGDFPYPIADPTDRLAVTLGMLDEEQKD 119
Qy 122 KGLPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSLQLTAKFP-VATPVDWTA 180
Db 120 PEVKTIKALFIISFDHKVRLSMFYPMTSGKNVDEILRTDLSLQTLRLKVVATPANWTP 179
Qy 181 GAKCCVVPNLAAEAQRLLPKGHEALQLPKGKPYLRLT 218
Db 180 GTKVMILPTVTDEEAHLFPKGFCKVSMPSGVNVRTT 217
RESULT 34
ABO68070
ID ABO68070 standard; protein; 222 AA.
XX AC ABO68070;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polypeptide #245.
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX DR N-PSDB; ABD01641.
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 16816; 455pp; English.
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-P. aeruginosa drugs, as templates for recombinant
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused
XX CC infection, and in detection of P. aeruginosa sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences ABO67826-
XX CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The

CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 222 AA;
Query Match 41.7%; Score 497.5; DB 7; Length 222;
Best Local Similarity 46.8%; Pred. No. 3.3e-47;
Matches 104; Conservative 34; Mismatches 71; Indels 13; Gaps 5;
Qy 1 MPNLGDSPPDFOAEALGAHFRHLYLGDGSGWVMSFHPNDFTPVCTTTELAELAVKLDQSF 60
Db 11 MSRLGDIADFPDQDS-SEGRIRLHFWLGDGSGWVLSFHPADFTPVCTTTELGFTAKLQDF 69
Qy 61 TKNCVLGFSNDLQSHREWAKDIWAYAGRSNLPFLVCDPNRELAASLGIMDPAEKD 120
Db 70 AQGVKVLALSDVPVESHKWIIDINETQTRVN--FPIADADRKVSELYDLIHPNAND 127
Qy 121 KKGPLTCRCVFFISPEKKLAASILYPATTGRNFAELRLVLDLSLQLTAKFPVATPVDWTA 180
Db 128 ----TLTVRSLSFIIDPNKKVRLIITYPASTGRNFNEILRLVIDSLQLTDEHKVATPANWED 183
Qy 181 GAKCCVVPNLAAEAQRLLPKGHEALQLPKGKPYLRLTDPD 221
Db 184 GDEWIVPSLKDDEEIKRRPKGYRAV-----KPYLRLTPOP 220
RESULT 35
ABB80958
ID ABB80958 standard; protein; 218 AA.
XX AC ABB80958;
XX DT 21-OCT-2002 (first entry)
XX DE Barley 1-Cys peroxiredoxin (HvPer1).
XX KW Oil palm; embryogenic-specific polypeptide; plant; OPEm1; apoptosis;
XX KW embryogenesis; molecular marker; antioxidant; antiaging; peroxiredoxin;
XX KW barley; 1-Cys peroxiredoxin; HvPer1.
XX OS Hordeum vulgare.
XX PN EP1217068-A2.
XX PD 26-JUN-2002.
XX PF 20-DEC-2001; 2001EP-00310705.
XX PR 20-DEC-2000; 2000AU-00002213.
XX PA (NAPA-) MALAYSIAN PALM OIL BOARD.
XX PI Abdullah MO, Kulaveerasingam H;
XX WPI; 2002-550405/59.
XX PT Novel isolated embryogenic-specific polypeptide from oil-palm, OPEm1, and
XX PT polynucleotides encoding them, useful as molecular markers for plant
XX PT embryogenesis and for inhibiting/retarding apoptosis in plant, animal
XX PS cells.
XX CC Disclosure; Fig 6; 41pp; English.
XX CC The invention relates to isolated embryogenic-specific polypeptide from
XX CC oil palm, OPEm1 and encoding polynucleotides. OPEm1 is present in plant
XX CC zygotic embryos or embryogenic callus and not present in non-embryogenic
XX CC tissue. OPEm1 can be expressed by standard recombinant technology. The
XX CC OPEm1 polypeptide is useful for modulating apoptotic processes in a cell.
XX CC The encoding polynucleotide is useful for detecting embryogenic plant
XX CC material. The OPEm1 polypeptide and polynucleotides act as molecular
XX CC markers for a plant physiological process, specifically plant
XX CC embryogenesis. The molecular markers enable embryogenic tissue to be

CC detected in vitro. They are also useful for inhibiting or retarding
 CC apoptotic processes in both plant and animal cells. OPEm1 has antioxidant
 CC activity, and thus is useful in tablet or cream as an antiaging agent.
 CC OPEm1 encodes a peroxiredoxin useful for the modulation of cellular
 CC apoptotic processes and is useful as an immunological agent to generate
 CC antibodies useful as diagnostic markers. The present sequence represents
 CC a barley 1-Cys peroxiredoxin (HvPer1) used in comparison studies with the
 CC oil palm OPEm1 polypeptide
 XX
 SQ Sequence 218 AA;

Query Match 41.5%; Score 495; DB 5; Length 218;
 Best Local Similarity 43.4%; Pred. No. 6.2e-47;
 Matches 95; Conservative 43; Mismatches 77; Indels 4; Gaps 4;
 QY 1 MP-LNLGDSPPDQAEALGAHEHRLHEYLGDSDGVGMFSPNDTPVCTTELAEAVKLQDS 59
 DB 1 MPGLTIGDTPVNLDELSTHGK-IRIHQVGVNGVILFSPGDFTPVCTTELAAMANYAKE 59
 QY 60 FTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEK 119
 DB 60 FEKRGVKLLGISDQVQSHKEWTKDIEAYKPGS-KVTYPIPADPDSRAIKQLNMVDPDEK 118
 QY 120 DKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLSLQLTAKFPVATPVDWT 179
 DB 119 DAQG-QLPSTLHIVGDKVKVLSFLYPSCTGRNMDVVRVNDLSLLTAAKHKVATPANWK 177
 QY 180 AGAKCCVVPNLAABEAAQRLLPKGHEALQLPSGKPYLRLT 218
 DB 178 PGECVWIAPGVSDBEAKMFPQGFETADLPSSKGYLRFT 216

RESULT 36

ADN21975
 ID ADN21975 standard; protein; 212 AA.

AC ADN21975;

XX 02-DEC-2004 (first entry)

DE Bacterial polypeptide #4628.

KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

DR WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 4628; 122pp; English.
 PS The invention relates to a recombinant DNA construct comprising a
 XX promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 212 AA;

Query Match 41.4%; Score 494.5; DB 8; Length 212;
 Best Local Similarity 45.9%; Pred. No. 6.8e-47;
 Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
 QY 1 MPLNLGDSPPDQAEALGAHEHRLHEYLGDSDGVGMFSPNDTPVCTTELAEAVKLQDSF 60
 DB 1 MSLRLGDIAPDFEQQS-SVGPIRFHEWLGDSGVLFSPADFTPVCTTELGLTAKLASEF 59
 QY 61 TTKKNCKLVGFSNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDPAEKD 120
 DB 60 EKRNVTIATLSVDSAESHKWKID--NETQAAVGFPIADGDKRVSELYDHIHPNANE 117
 QY 121 KKGLPLTCRCVFFISPEKKLAASILYPATTGRNFAEILRVLSLQLTAKFPVATPVDWTA 180
 DB 118 ----TLTVRSFVIDPKKVRLLIYYPASTGRNFDVLRVIDLSLQLTDSHVSATPGNWKQ 173
 QY 181 GAKCCVVPNLAABE-AQRLLPKGHEALQLPSGKPYLRLTDPD 221
 DB 174 GDDVWIVPSLKDDEIIKQKFKGYKAL-----RPYLRMTPQP 210

RESULT 37

ADN24733
 ID ADN24733 standard; protein; 212 AA.

XX ADN24733;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #7386.

KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

```
PD 18-DEC-2003.
XX
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 7386; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plants with
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 212 AA;
Query Match 41.4%; Score 494.5; DB 8; Length 212;
Best Local Similarity 45.9%; Pred. No. 6.8e-47;
Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
Qy 1 MPLNLGDSFPDFOAEALGAEHFRLHEYLGDGSGVMFSDHNDFTPVCTTELAELAVKLQDSF 60
Db 1 MSLRLGDIAPDFEQQS-SVGPPIRHEWLGDGSGVLFSDHNDFTPVCTTELGTLAKLASEF 59
Qy 61 TKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEKD 120
Db 60 EKRNVKTIALSVDAESHKGIWKDI--NETQANVGFPILADGRKVSLEYDMIHPNANE 117
Qy 121 KKGGLPLTCRCVFFISPEKLAASILYPATTTGRNFAELRLVLDLSQLTAKFPVATPVDTWA 180
Db 118 ----TLTVRSILFVIDPKKVRLLIITYPASTGRNFDEVLRLVLDLSQLTDSHVSATPGNWKQ 173
Qy 181 GAKCCVVPNLAAEE-AQRLLPKGHEALQLPSGKPYRLRLTDPD 221
Db 174 GDDVIVVPSLKDDEIIKQKPKGYKAL-----RPLYRLMTPOP 210
XX
XX RESULT 38
XX ADA34041
XX ID ADA34041 standard; protein; 216 AA.
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XX ADA34041;
XX
XX 20-NOV-2003 (first entry)
XX
XX Acinetobacter baumannii protein #1202.
XX
XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX
XX Acinetobacter baumannii.
XX
XX US6562958-B1.
XX 13-MAY-2003.
XX
XX 04-JUN-1999; 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton G, Bush D;
XX
XX WPI; 2003-576092/54.
XX N-PSDB; ADA29915.
XX
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, to detect the presence of
XX A. baumannii and other Acinetobacter species in a sample, in screening
XX compounds for the ability to interfere with the A. baumannii life cycle
XX or to inhibit A. baumannii infection, and as biocontrol agents for
XX plants. The present sequence represents the amino acid sequence of an A.
XX baumannii protein.
XX
XX SQ Sequence 216 AA;
Query Match 41.4%; Score 494.5; DB 6; Length 216;
Best Local Similarity 45.7%; Pred. No. 7e-47;
Matches 102; Conservative 37; Mismatches 69; Indels 15; Gaps 6;
Qy 1 MPLNLGDSFPDFOAEALGAEHFRLHEYLGDGSGVMFSDHNDFTPVCTTELAELAVKLQDS 59
Db 4 MTLRLGDTAPDFQESSEGTINF--YDFLGDGSGVILFSDHNDFTPVCTTELGTLAKLDE 61
Qy 60 FTKKNCKLVGSCNDLQSHREWAKDIMAYAGRSNLPFLVCDPNRELAASLGIMDPAEK 119
Db 62 FEKRVNKATLSVDDVESHKGIWKDI--FPIADKDKRVKVSLEYGFIHFNAS 119
Qy 120 KKGGLPLTCRCVFFISPEKLAASILYPATTTGRNFAELRLVLDLSQLTAKFPVATPVDTW 179
Db 120 E----TLTVRSILFVIDPKKVRLLIITYPASTGRNFDEVLRLVLDLSQLTDKHKVATPANWQ 175
Qy 180 AGAKCCVVPNLAAEE-AQRLLPKGHEALQLPSGKPYRLRLTDPD 221
Db 176 QGDDVIVVPSLKDDEIIKQKPKGYTTV-----KPYRLMTPOP 213
XX
XX RESULT 39
XX ADN22014
XX ID ADN22014 standard; protein; 212 AA.
XX
XX AC ADN22014;
XX
```

DT 02-DEC-2004 (first entry)
XX Bacterial polypeptide #4667.
DE Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
PN 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
PR (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 4667; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 212 AA;
SQ Query Match 41.3%; Score 493.5; DB 8; Length 212;
Best Local Similarity 45.9%; Pred. No. 8.8e-47;
Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
QY 1 MPLNLGDSFPDQAEALGAEHRLHEYLGDWGMFSDHNDFTFVCTTELAEAVKLQDSF 60
DB 1 MSLRLGDIADPDERQS-SVGPFRFHEWLGDWGMFLSDHNDFTFVCTTELGLAKLAGEF 59

QY 61 TKKCKLVGFCSCNDLQSHREWAKDIMAYAGRSNLPFPLVCDPNRELAASLGIMDAEKD 120
DB 60 EKRNVTKTALSVDSAESHKEWKID1--NETQAANGVFPILADGDRKVSLEYDMHPNANE 117
QY 121 KKGLPLTCRCVFFISPEKLAASILYPATTGRNFABILRVLDLSQLTAKFPFVATPVDWTA 180
DB 118 ----TLTVRSLVFIDPKKKVRLIIYPASTGRNFDEVLRLVDSLQJTDHSHVATPQWKKQ 173
QY 181 GAKCCVVPNLAAEE-AQRLLPKGHEALQLPSGKPYLRLPDP 221
DB 174 GDVVIVPSLKDDEIIKQKPKGYKAL-----RPVLRMTQP 210
RESULT 40
ADN24773
ID ADN24773 standard; protein; 212 AA.
XX ADN24773;
AC ADN24773;
XX 02-DEC-2004 (first entry)
DT Bacterial polypeptide #7426.
DE Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX US2003233675-A1.
PN 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 7426; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 212 AA;
SQ Query Match 41.3%; Score 493.5; DB 8; Length 212;
Best Local Similarity 45.9%; Pred. No. 8.8e-47;
Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;

CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 212 AA;

Query Match 41.3%; Score 493.5; DB 8; Length 212;
Best Local Similarity 45.9%; Pred. No. 8.8e-47;
Matches 102; Conservative 37; Mismatches 70; Indels 13; Gaps 5;
Qy 1 MPLNLGDSFPDFOAEALGAEHFRLHEYLGDWSGVMFSGHPNDFTVCTTELAAEAVKLQDSF 60
Db 1 MSLELGDIAPDFFERQS-SVGFIRFEHWLGDWSGVLFSHPADFTVCTTELGLTAKLAGEP 59
Qy 61 TKNCKLVGFSCNDLQSHREWAKDIMAYAGRSGNLPFLVCDPNRELAASLIGIMDPAEKD 120
Db 60 EKRNVKTIALSVDSAESHKWIKDI--NETQANVGFPILADGDRKVSLEYDMHPNANE 117
Qy 121 KKGLPLTCRCVFFISPEKLAASILYPATTGRNPABILRVLDLSLQLTAKFPVATPVDWTA 180
Db 118 ----TLTVRSILFVIDPKKVRLLIITYPASTGRNPFDEVLRVIDSLQLTDSHVSATPGNWKQ 173
Qy 181 GAKCCVVPNLAAEE-AORLLPKGHEALQLPSGKPYLRLTDPD 221
Db 174 GDDVVIVPSLKDEEIIKQKFPKGYKAL-----RPLYRWTPQP 210

Search completed: October 28, 2005, 21:52:56
Job time : 178 secs

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